QUANTIFICATION OF THE GENETIC VARIATION IN AFRICAN BERMUDAGRASS (*CYNODON TRANSVAALENSIS*) FOR SELECTED TRAITS

By

KEVIN EUGENE KENWORTHY

Bachelor of Science
Texas Tech University
Lubbock, Texas
1994

Master of Science
Texas Tech University
Lubbock, Texas
1996

Submitted to the Faculty of the
Graduate College of the
Oklahoma State University
in partial fulfillment of
the requirements for
the Degree of
DOCTOR OF PHILOSOPHY
July, 2004

QUANTIFICATION OF THE GENETIC VARIATION IN AFRICAN BERMUDAGRASS (*CYNODON TRANSVAALENSIS*) FOR SELECTED TRAITS

Dissertation Approved:

C. M. Taliaferro
Dissertation Advisor

Dennis L. Martin

Jeff Anderson

Brett F. Carver

Alfred Tabogi
Dean of the Graduate College

AKNOWLEDGEMENTS

I want to express my sincere appreciation to my major professor, Dr. Charles Taliaferro, for his guidance during my graduate work. He was very accommodating with regards to my family and my current position at Tarleton State University. He allowed me the freedom to work according to my own schedule. My appreciation extends to my other committee members, Dr. Brett Carver, Dr. Dennis Martin, and Dr. Jeff Anderson, whose encouragement and guidance kept me on my toes. I have learned from each of them, and hope to continue these relationships through my career.

I want to thank Rose Edwards, and Gary and Sharon Williams for their help in the greenhouse and field. This project would not have been possible, and therefore; my Ph.D. without their willingness to always lend a hand. Also Yanqi Wu, what a great friend and colleague I gained from this experience. I look forward to a long friendship, both personal and professional.

This thesis is dedicated to my family. First, to my wife Brandi, for her support, encouragement, and love during this difficult process, we made it. I love you and look forward to being able to spend time with you. To our children, Gracie and Jaxon, you have given me a whole new perspective on life, and always something to smile about. Brandi's parents have been a great support and help. Completion of the Ph.D. would not have been possible without Sharon and Roger or Ken and Charla. Sharon, you went above the call of duty watching

grandchildren almost weekly and taking time from your own activities to help. To my own parents, Joe and Becky, who also helped enormously, and have always supported my endeavors with a go-for-it attitude.

This thesis is in memory of my Mother, Rebecca Gene Noblitt Kenworthy (1943 – 2004). Mom, looking back I realize that everything I am, is because of how you lived and viewed life. You taught me to be curious and investigative; that being positive will get you through anything, and a love for outdoors and exploring. You will always be my life's example. I am truly blessed to have had you as a Mother. I miss you more every day.

TABLE OF CONTENTS

CHAPTER PAGE

APPENDICES PAGE

LIST OF TABLES

LIST OF FIGURES

CHAPTER I

INTRODUCTION

Objective

The *Cynodon* genus is comprised of nine bermudagrass species. Two species, *C. dactylon* (L.) Pers. var. *dactylon* and *C. transvaalensis* Burtt-Davy are economically important to the turfgrass industry. *Cynodon dactylon* var. *dactylon* is often referred to as common bermudagrass due to its cosmopolitan distribution throughout the warmer regions of the world. Genetic variation in common bermudagrass has been well documented with respect to growth habits that range from very small, fine turf types to more robust forage types (Harlan et al., 1970c; Harlan and de Wet, 1969). Harlan and de Wet (1969) stated that the morphological variation within var. *dactylon* is enormous. Baltensperger and colleagues estimated the heritability of selected traits in *C. dactylon* var. *dactylon*, documenting the enormous amount of variation and demonstrating the potential for improvement of traits studied through conventional breeding methods (Wofford and Baltensperger, 1985; Coffey and Baltensperger, 1989; Cluff and Baltensperger, 1991). In contrast, little is known regarding the kinds and magnitudes of genetic variation in *C. transvaalensis* (Taliaferro, 1995). *Cynodon transvaalensis*, known as African bermudagrass, is indigenous to the Transvaal region of South Africa. Plants of African bermudagrass are typically

characterized as small, narrow leafed, and yellow-green in color (Harlan et al., 1970a; Harlan et al., 1970c). Plants are further described as being very uniform in appearance (de Wet and Harlan, 1971). However, variation has been observed for morphological and adaptation traits for segregating populations of *C. transvaalensis* (Taliaferro, 1992; Gerken, 1994).

Even though common bermudagrass and African bermudagrass are morphologically distinct from each other, they easily hybridize. African bermudagrass, a diploid (2n = 2x = 18), crossed with common bermudagrass, a tetraploid (2n = 4x = 36), produces a sterile, triploid, interspecific hybrid (2n = 3x = 27) (Harlan et al., 1970a; de Wet and Harlan, 1971; Burton, 1977; Burton, 1991). These triploid hybrids first came into importance through the work of Dr. Glenn Burton at the University of Georgia Coastal Plain Experiment Station, Tifton, Georgia in the 1950's and 60's. Dr. Burton was the first to make controlled crosses between *C. dactylon* var. *dactylon* and *C. transvaalensis* in an attempt to produce superior turf type bermudagrass plants. The hybrids released from this program are the most important and widely used turfgrasses throughout the warmer climates of the world (Burton, 1973; Burton, 1977; Burton, 1991). The widespread use of relatively few vegetatively propagated bermudagrass cultivars increases susceptibility to damage from new pests (Taliaferro, 1995). As well, many subsequent and newly released cultivars of bermudagrass have arisen from mutations, natural and induced, of currently used cultivars (Burton, 1973; Burton, 1977; Burton, 1985; Burton, 1991; Beard, 2000). Therefore, while a greater number of cultivars are commercially available, most of them share a

common genetic background that still results in worldwide susceptibility to damaging pests.

The purpose of this study is to quantify the genetic variation for selected traits in *C. transvaalensis.* This will allow for determination of heritability estimates. Quantification of this variation will provide breeders with information regarding the potential for improvement of *C. transvaalensis* and hybrids of *C. dactylon* var. *dactylon* and *C. transvaalensis.*

Literature Review

The genus *Cynodon,* having nine species, is a member of the tribe Chlorideae. Three of the species are subdivided into varieties: *C. dactylon* into five varieties, *C. incompletes* into two varieties, and *C. nlemfuensis* into two varieties. The different species contain plants ranging from small, diminutive types useful as turf, to more robust forms suitable for grazing and hay production. They also vary according to areas and range of distribution and moisture requirements for survival (Harlan and de Wet, 1969; Harlan et al., 1969, Harlan et al., 1970c; Harlan, 1970).

Cynodon transvaalensis Distribution and Adaptation

Cynodon transvaalensis, commonly referred to as African bermudagrass, is endemic to South Africa, has a very small natural distribution, and is found in moist areas within the southwestern Transvaal area, Orange Free State, and the northern part of the central Cape Province of South Africa (Harlen et al., 1970a;

Harlan et al., 1970c). African bermudagrass can usually be found growing in damp areas around surface water and stream banks (Harlen et al., 1970b).

Cynodon transvaalensis is adapted to much cooler climates and is more winter hardy than is implied by its natural distribution (Harlan et al, 1970a). 'Uganda' and 'Florida,' are among the earliest of the African cultivars and have been widely distributed around the world. Their confirmed cold tolerance is approximately 39 °N latitude in the United States (Taliaferro, 1992; Taliaferro, 2001).

Use of C. transvaalensis has been limited due to the following: 1) increased use of water and nutrients, 2) tendency to thatch, 3) lack of a dark green color, 4) purpling under cooler temperatures, and 5) a decline in turf quality as a result of chronic heat stress. It is not known if these limitations are characteristics of the species as a whole or just the relatively few available varieties (Taliaferro, 1992).

Cynodon transvaalensis Botanical Characteristics

Cynodon transvaalensis plants are characterized as low-growing, turf type bermudagrasses (Hanna, 1986). They can reproduce vegetatively, through propagation of stolons and rhizomes, or sexually, through seed production. Because plants of *C. transvaalensis* are self-incompatible, different genotypes must be planted together in order to set seed (Harlan et al., 1970b).

Plants are further described as having fine-textured, hairy, erect leaves, and a yellowish green color. Leaf blades can be as wide as 1.5 mm, and as long as 4 cm. Stolons are slender with shortened internodes and can be reddish in

color. Rhizome growth is shallow compared to other *Cynodon* species (Juska and Hanson, 1964; Harlan et al, 1966; Harlan et al., 1970b; Harlan et al., 1970c). Cynodon transvaalensis has folded vernation. The ligule is ciliolate membranous and ranges in length from 0.1 to 0.3 mm. The collar is continuous. Auricles are absent from *C. transvaalensis*. The leaves contain three primary nerves (Hurcombe, 1947; Royal Botanic Gardens, Kew, 1999).

Flowering culms can be as high as 10 cm (Juska and Hanson, 1964). Inflorescences are small, with one whorl, and have 1 to 5 (normally 2) racemes that range from 1 to 2 cm long. Spikelets are loosely arranged and vary in length from 2 to 4 mm (Hurcombe, 1947; Juska and Hanson, 1964; Harlan et al., 1966; Harlan et al., 1970b; de Wet and Harlan, 1971). Flowers are perfect, and have one pistil and three anthers (Taliaferro, 2001). Glumes are ¾ the length of the spikelet, and lemmas are pointed and slightly hairy on the keel (Harlan et al., 1966; Harlan et al., 1970b). Flowering is prolific during the spring and fall with few seedheads occurring during the summer months. Seed set of *C. transvaalensis* has been characterized as good; however, shattering of seed at maturity is quite common (Taliaferro, 2001).

Cytology and Cytological Relationships of *Cynodon transvaalensis*

The first reports of chromosome numbers in *C. transvaalensis* showed it to be a diploid, 2n=2x=20, that has a base chromosome number of 10 (Hurcombe, 1947). Subsequent examinations confirmed a base chromosome number of 9 for *Cynodon*. Ploidy in the genus ranges from diploid, 2n=2x=18, to hexaploid,

2n=6x=54. *Cynodon transvaalensis* is a diploid and *C. dactylon* var. *dactylon* is a tetraploid (Forbes and Burton, 1963; Powell et al., 1968; Harlan et al., 1970a).

A cytogenetic analysis was conducted by Harlan et al. (1970a) to determine the relationships among species and varieties of *Cynodon*. *Cynodon transvaalensis* is genetically linked to *C. dactylon* var. *dactylon*, but morphologically the two species are distinct; however, they easily hybridize in nature and under controlled conditions. *Cynodon transvaalensis* has also been crossed with *C. dactylon* var. *coursii*, var. *elegans* (a tetraploid), and with *C. nlemfuensis* var. *nlemfuensis* (a diploid) (de Wet and Harlan, 1970). These relationships of *C. transvaalensis* to other *Cynodon* taxa were summarized by Harlan et al. (1970a), and are as follows: 1) some affinity for *C. nlemfuensis*, and 2) a close relationship to *C. dactylon*. They stated that the relationship between *C. transvaalensis* and *C. dactylon* is significant enough that *C. transvaalensis* could be changed from species status to a variety of *C. dactylon*. However, due to the distinct morphological differences between the two, the status of *C. transvaalensis* was left the same (Harlan, et al., 1970a). Caetano-Anolles et al. (1995) studied the relationship between *C. transvaalensis* and *C. dactylon* var. *dactylon* using DNA amplification fingerprinting. Results showed distinct DNA clusters between *C. transvaalensis* and *C. dactylon* var. *dactylon* with interspecific hybrids forming an intermediate cluster between the two species or combining with the *C. dactylon* var. *dactylon* genotypes.

Importance of *Cynodon transvaalensis*

The importance of *C. transvaalensis* primarily relates to its use as a parent along with *C. dactylon* var. *dactylon* to produce sterile, interspecific triploid hybrids (Burton, 1973; Burton, 1977; Hanna, 1986; Burton, 1991; Taliaferro, 1992, Taliaferro, 1995). These bermudagrass hybrids are the most important warm-season turfgrasses worldwide. The key to the development of these hybrids is the utilization of germplasm. As of April 2001, the GRIN (Germplasm Resources Information Network) database showed that 15 accessions of C. transvaalensis are in NPGS (National Plant Germplasm System). Two of these accessions, Uganda and Florida, have seen limited use in the U.S. as direct increases of vegetative material (Juska and Hanson, 1964).

Dr. Glenn Burton, University of Georgia Coastal Plain Experiment Station, Tifton, Georgia, began breeding bermudagrass for turf in 1946. He was the first to make crosses between *C. dactylon* var. *dactylon* and *C. transvaalensis* and to evaluate the hybrids for improved turfgrass characteristics. Interspecific, triploid hybrids developed and released from this program include 'Tiffine,' 'Tifgreen,' 'Tifway,' 'Tifdwarf,' 'Tifway II,' 'Tifgreen II,' 'TifSport,' and 'Tif-Eagle' (Burton, 1973, Burton, 1977, Hanna, 1986, Burton, 1991, Alderson and Sharp, 1993; Hanna et al., 1997; Hanna and Elsner, 1999). Other hybrid cultivars developed and released include 'Everglades,' ' Santa Ana' (California AES), 'Sunturf' (Alabama AES, Arkansas AES, Oklahoma AES, and South Carolina AES), 'Bayshore,' 'Ormond,' 'Midfield' (Kansas AES and Oklahoma AES), 'Midiron' (Kansas AES), 'Midlawn' (Kansas AES and Oklahoma AES), 'Midway' (Kansas

AES), 'Pee Dee 102' (South Carolina AES) 'Floradwarf' (Florida AES), 'MS-Supreme' (Mississippi AES), 'Champion' (Coastal Turf, Inc), 'Mini Verde' (H&H Seed Co./Turfgrass America), 'Baby' (Bladerunner Farms), and 'Patriot' (Oklahoma AES). Everglades, Santa Ana, Sunturf, Bayshore, Ormond (Juska and Hanson, 1964), and Tifway (Burton, 1977; Alderson and Sharp, 1993) are the result of naturally occurring crosses between *C. dactylon* var. *dactylon* and *C. transvaalensis.* Tifdwarf, Tifway II, Tifgreen II, Pee Dee 102 (Burton, 1973, Burton, 1977, Hanna, 1986, Burton, 1991, Alderson and Sharp, 1993), TifSport, TifEagle (Hanna et al., 1997; Hanna and Elsner, 1999; Beard, 2000), Floradwarf (Beard, 2000), MS-Supreme (Krans et al., 1999; Beard, 2000), Champion (Beard, 2000), and Mini Verde (Caldwell, personal communication) are the result of naturally occurring mutations or man-induced mutants from previously released material. The remaining cultivars, Tiffine, Tifgreen (Burton, 1973, Burton, 1977, Hanna, 1986, Burton, 1991, Alderson and Sharp, 1993), Midfield, Midiron, Midlawn, Midway (Alderson and Sharp, 1993), and Patriot (Taliaferro, personal communication) are the result of controlled crosses. The exact pedigree of Baby is not known (Engelke, personal communication;).

The cultivars with the most acreage under management are Tifgreen, Tifdwarf, and Tifway. Taliaferro (1995) stated that in turf, widespread use of relatively few clonally propagated cultivars in the USA increases susceptibility to damage from new pests. This is further compounded because many newer varieties are natural or man-induced mutants selected from previously released material. Therefore, many cultivars share very similar genetic backgrounds.

This is illustrated by the development of the following cultivars. Tifgreen, released in 1956, is an F1 hybrid between a *C. dactylon* var. *dactylon* plant selected at Charlotte Country Club, Charlotte, NC and a *C. transvaalensis* plant selected from East Lake Golf Course in Atlanta, GA. Tifdwarf, released in 1965, is a natural, dwarf mutant that occurred in Tifgreen (Burton, 1973, Burton, 1977, Hanna, 1986, Burton, 1991, Alderson and Sharp, 1993; Hanna and Elsner, 1999). As well, recently released cultivars Mini Verde (Caldwell, personal communication), Champion (Beard, 2000), Floradwarf (Beard, 2000), and MS Supreme (Krans et al., 1999; Beard, 2000) are natural mutants selected out of old greens of Tifgreen or Tifdwarf. The intended use for all of these cultivars is for golf course putting greens; therefore, if a pest develops that is damaging to one cultivar it is likely that all related cultivars used on greens will be susceptible. This presents a situation for golf courses in warmer regions similar to the southern corn leaf blight epidemic of 1970. During this time many corn (*Zea mays*) hybrids contained the Texas cytoplasmic male sterility gene that was susceptible to the causal fungus, *Bipolaris maydis*. This epidemic was severe because many hybrid cultivars shared a common genetic background (Agrios, 1988). To alleviate or avoid this situation Tif-Eagle was developed and released for use on golf course putting greens. Its genetic background differs from the other cultivars used on greens. However, it was selected from a population of plants produced by irradiating vegetative material of Tifway II (Hanna, 1996; Hanna and Elsner, 1999). Tifway II is a selection from irradiated Tifway (Burton, 1985), and these two cultivars make up the majority of golf course fairways and

sports fields planted to improved turf-type bermudagrasses. Therefore, the use of Tif-Eagle also results in potential for significant damage as a result of new pests.

The reduction of this risk can only be achieved through the development of hybrid cultivars with a broader genetic base. Development of superior cultivars will require extensive knowledge of available germplasm to select parents with desirable characteristics (Taliaferro, 1995). de Wet and Harlan (1971) described populations of *C. transvaalensis* as being very uniform based on morphological observations. However, Taliaferro (1992) and Gerken (1994) have observed and documented the occurrence of variation related to morphological and adaptation traits in segregating populations of *C. transvaalensis*. Taliaferro (1992) screened large numbers of *C. transvaalensis* plants for their tolerance to putting green conditions. Variation was observed within this population for establishment rate, winter survivability, texture, density, color, and mowing height tolerances. Gerken (1994) evaluated six experimental accessions of *C. transvaalensis* along with Uganda and Tifgreen for putting green characteristics. Significant differences were observed for rate of establishment, clipping yield, leaf blade angles, root mass, shoot density, visual density, spring greenup, stimpmeter readings, color, and turf quality. Taliaferro (1992) explained that if the variation observed for these traits is heritable, there exists potential for breeding *C. transvaalensis* to develop cultivars, or as a source of elite parents to produce new triploid, interspecific hybrid turf-type bermudagrasses.

Estimates of Genetic Parameters

Information related to phenotypic variation as a result of genetic and environmental forces is essential for the plant breeder to make decisions regarding the use of resources and the expected gains in response to selection. Because genotypic and environmental factors govern the expression of the phenotype, it is important to determine the level that genotypic and environmental effects have on the expressed phenotype (Hallauer and Miranda, 1981). Estimates of genetic variance and heritabilities are useful for all aspects of plant breeding (Dudley and Moll, 1969).

Heritability is a measure of the effect that selection can have on a phenotypic trait. Broad sense heritability is the ratio of total genetic variance to phenotypic variance. Narrow sense heritability is the ratio of additive genetic variance to phenotypic variance. Phenotypic variance is the total variance in a phenotypic trait among individual members of a population. Genetic variance is the portion of the phenotypic variance attributed to differences in genotype among phenotypes. Genetic variance can be subdivided into additive genetic variance, dominance genetic variance, and epistatic genetic variance. Additive genetic variance is the magnitude of the genetic variance that results from the additive action of genes (or the average effect of substituting one allele for another). Dominance genetic variance is the portion of genetic variance that results from the dominance effects (one allele partially or completely masks the expression of another allele) of alleles affecting the trait. It can also be stated that the dominance variance is the remaining variance after subtracting the

additive genetic variance from the total within-locus variance. The epistatic genetic variance is the remaining genetic variance after subtracting the total within-locus variance. Genetic variance due to epistasis occurs when the total within-locus genetic variance fails to account for the total variation among genotypes (Dudley and Moll, 1969; Hartl, 1991).

Estimating genetic variance components requires the use of an appropriate mating and environmental design (or system used to develop progenies). When choosing a mating design, it is best to select the simplest design that will provide the breeder with the necessary information. A one-factor design is appropriate to determine the existence of genetic variability; however, in order to separate additive and dominance variance, a two-factor design is required (Dudley and Moll, 1969). Two-factor designs include the Diallel Cross, and Designs I, II, and III, as described by Comstock and Robinson (1952). When using a two-factor design, it is assumed that epistasis is absent. For estimation of epistatic variance, a more complex design is required (Dudley and Moll, 1969).

Estimates of the components of genetic variances can be equated to covariances among relatives if the parents are random members of the genetic population and if experimental errors are independent. Conversion of the covariances between relatives into additive, dominance, and epistatic genetic variances requires a thorough understanding of the genetic population being sampled. For example, restrictions related to the genetic population include: 1) Mendelian inheritance occurs, 2) no environmental correlations among progenies, 3) the progenies are not inbred and can be considered random

members of some non-inbred population, and 4) linkage equilibrium (Cockerham, 1961; Cockerham, 1963).

By following these restrictions, estimates of genetic variance components can be obtained. These estimates can then be used to estimate heritability, and to predict gain made possible from various types of selection. The major difference between the design used for experiments of this type and other agronomic experiments is that the characters of interest are expressed as variances rather than means. The mating design must be arranged so sets of progenies can be randomly assigned to the blocks in a way that will allow an independent estimate of the variances of interest from an analysis of each block (Dudley and Moll, 1969).

Baltensperger and colleagues estimated the heritability of several traits in populations of *C. dactylon* var. *dactylon*. Estimated traits included various turfgrass characteristics such as density, leaf length, leaf width, stolon internode length, color, vigor, turf quality, and seedhead production (Wofford and Baltensperger, 1985). Coffey and Baltensperger (1989) determined heritability estimates for chlorophyll content, color, turf quality, density, and clipping weight for bermudagrass grown under shaded conditions. Cluff and Baltensperger (1991) estimated heritability for seed yield and seed yield components in bermudagrass. Results of these studies indicated that the evaluated traits are heritable and that improvement is possible through selection. Such information is not available for *C. transvaalensis*.

Design II Mating Scheme

Comstock and Robinson (1948) first described the Design II mating scheme. The scheme uses different sets of male and female parents, and is useful for species in which the female can generate progenies by more than one male (i.e. multi-flowered plants). For instance, progenies are obtained from each female for each male. This results in a set of biparental progenies in which each male is crossed with each female. As an example, if eight parents are randomly selected to produce a set of progenies, then four parents will be randomly designated as females and four randomly designated as males. Crossing each female with each male produces a total of 16 crosses for a set.

Hallauer and Miranda (1981) described the analysis of the Design II. The above procedures result in an analysis of variance (AOV) table with sources of variation for males, females, and the male by female interaction. In the model I analysis, the expected mean squares for males and females are equal to the general combining ability (GCA = average performace of the progeny of an individual when mated with a series of genotypes), and the male X female expected mean squares is equal to the specific combining ability (SCA = performance of the progeny from the cross of two specific genotypes in comparison to the average performance of progenies from the mating of a series of genotypes in all possible combinations). As well, appropriate F-tests can be performed to test for differences among males, females, and for the interactions of males and females.

For analysis of the model II, estimates of components of genetic variance are provided by the covariances of relatives. These estimates of variance components characterize the population from which the parents were a random sample.

The Design II breeding method has the following advantages when estimates of variance components are needed for a reference population: (1) more parents can be involved per available resources, (2) two independent estimates of additive variance are available, (3) an estimate of the dominance variance can be determined from the mean squares, and (4) more parents can be used by subdividing them into sets.

The AOV for parents grouped into sets will include a source of variation for sets along with the other sources as stated above. For this arrangement, an analysis is conducted on each set, and sums of squares and degrees of freedom are pooled over sets.

Use of the Design II allows for estimates of genetic variance components to be made if it is assumed that the population is in linkage equilibrium with no epistasis. Heritability estimates can be calculated from additive variance estimates from the male and female variance components. This provides repeated (male and female) estimates of heritability. Estimates of heritability for individual plants can also be calculated if data is collected on individual plants. Therefore, the Design II is a useful breeding method for providing estimates of genetic variances in a population.

Use of Design II

Pixley and Frey (1991) developed an oat (*Avena sativa* L.) population to determine the combining ability for various agronomic traits. They concluded that general combining ability accounted for most of the variability in test weight, grain yield, harvest index, date of heading, and plant height. Specific combining ability was also significant for all traits measured.

Holland and Munkvold (2001) determined that oat grain yield, 100-seed weight, test weight and AUDPC (area under the disease progress curve) were heritable under rust-inoculated (*Puccinia coronata* Corda var. *avenae*) and fungicide-treated plots. They concluded that these traits should respond well to selection.

Johnson et al. (1996) determined the inheritance of several root traits in alfalfa (*Medicago sativa* L.). They calculated moderate to high heritability estimates for taproot diameter, lateral root number, lateral root diameter, lateral root position, and fibrous root mass indicating that improvement for these traits is possible with selection. No genetic variance was found to exist for percent determinate taproot or determinate taproot position indicating that selection will not improve these two traits.

Ortiz and Golmirzaie (2002) compared the use of North Carolina mating designs I and II to determine the relative advantages of the designs for analysis of the quantitative genetics of tuber yield in tetrasomic potato. They concluded that the design I mating scheme was the more appropriate method for this type of research in tetrasomic potato.

Objective

Estimate the genetic variance and heritability of selected traits in *Cynodon transvaalensis*.

Literature Cited

Alderson, J., and W.C. Sharp. 1993. Grass varieties in the United States, 2ed. U.S. Dep. Agric., Agric. Res. Ser., Agric. Handbook no. 170. U.S. Gov. Print. Office, Washington, DC.

Agrios, G.N. 1988. Plant pathology, 3rd ed. Academic Press, Inc. San Diego, CA.

Beard, J.B. 2000. The new high density bentgrass and bermudagrass cultivars for very closely mowed putting greens. Club Managers Assoc. of America 73rd Annual Conference, Atlanta, GA. 193-207.

Bell, G.E., D.L. Martin, S.G. Wiese, D.D. Dobson, M.W. Smith, M.L. Stone, and J.B. Solie. 2002. Vehicle-mounted optical sensing: an objective means for evaluating turf quality. Crop Sci. 42:197-201.

Burton, G.W. 1973. Breeding bermudagrass for turf. p. 18-22. *In* E.C. Roberts (ed.). Proc. 2nd Int. Turfgrass Res. Conf. Intl. Turfgrass Soc., Blacksburg, VA.

Burton, G.W. 1977. Better turf means better golf: the bermudagrass- past, present, and future. U.S. Golf Assoc. Green Section Record. March:5-7.

Burton, G.W. 1985. Registration of Tifway II bermudagrass. Crop Sci. 25:364.

Burton, G.W. 1991. A history of turf research at Tifton. U.S. Golf Assoc. Green Section Record. 29(3):12-14.

Caetano-Anollés, G., L.M. Callahan, P.E. Williams, K.R. Weaver, and P.M. Gresshoff. 1995. DNA amplification fingerprinting analysis of bermudagrass (Cynodon): genetic relationships between species and interspecific crosses. Theor. Appl. Genet. 91:228-235.

Cluff, G.J., and A.A. Baltensperger. 1991. Heritability estimates for seed yield and seed yield components in bermudagrass. New Mexico Agric. Exp. Stn. Bull. 759.

Cockerham, C.C. 1961. Implications of genetic variances in a hybrid breeding program. Crop Sci. 1:47-52.

Cockerham, C.C. 1963. Estimation of genetic variances. *In* W.D. Hanson and H.G. Robinson (ed.) Statistical genetics and plant breeding Publ. 982 Nat. Acad. Sci. – Nat. Res. Council. Washington, D.C., p. 53-93.

Coffey, B.N., and A.A. Baltensperger. 1989. Heritability estimates for selected turfgrass characteristics of bermudagrass evaluated under shade. p. 117-119. *In* H. Takatoh (ed.). Proc. Int. Turfgrass Res. Conf., 6th, 31 July – 5 Aug. 1989, Tokyo, Jpn. Intl. Turfgrass Soc. and Jpn Soc. Turfgrass Sci., Tokyo.

Comstock, R.E., and Robinson, H.F. 1948. The components of genetic variance in populations of biparental progenies and their use in estimating the average degree of dominance. Biometrics. 4:254-266.

Comstock, R.E., and Robinson, H.F. 1952. Estimation of average dominance of genes. *In* J. Gowen (ed.). Heterosis. Iowa State Univ. Press, Ames, IA. P. 494-516.

de Wet, J.M.J., and J.R. Harlan. 1970. Biosystematics of *Cynodon* L.C. Rich. (Gramineae). Taxon. 19(4):565-569.

de Wet, J.M.J., and J.R. Harlan. 1971. South African species of *Cynodon* (Gramineae). J. S. Afr. Bot. 37(1):53-56.

Dudley, J.W., and R.H. Moll. 1969. Interpretation and use of estimates of heritability and genetic variances in plant breeding. Crop Sci. 9:257-262.

Fehr, W.R. 1991. Maximizing genetic improvement. *In* Principles of Cultivar Development. Macmillian Publishing Co. P. 219-235.

Forbes, I., and G.W. Burton. 1963. Chromosome numbers and meiosis in some *Cynodon* species and hybrids. Crop Sci. 3:75-79.

Gerken, D.A. 1994. Evaluation of African bermudagrass as a putting surface. M.S. Thesis. Dept. Horticulture and Landscape Architecture, Oklahoma State University, Stillwater, OK.

Hallauer, A.R., and J.B. Miranda, Fo., 1981. Quantitative genetics in maize breeding. Iowa State Univ. Press, Ames, IA.

Hanna, W.W. 1986. A bermudagrass Primer and the Tifton bermudagrass. U.S. Golf Assoc. Green Section Record. Jan./Feb.:11-13.

Hanna, W.W. 1996. TW-72: A potential new bermudagrass for golf greens. U.S. Golf Assoc. Green Section Record. Sept./Oct.:11-12.

Hanna, W.W., and J.E. Elsner. 1999. Registration of 'Tifeagle' bermudagrass. Crop Sci. 39:1258.

Hanna, W.W., R.N. Carrow, and A.J. Powell. 1997. Registration of 'Tift 94' bermudagrass. Crop Sci. 37:1012.

Harlan, J.R. 1970. *Cynodon* species and their value for grazing and hay. Herbage Abstracts. 40(3):233-238.

Harlan, J.R., and J.M.J. de Wet. 1969. Sources of variation in *Cynodon dactylon* (L). Pers. Crop Sci. 9:774-778.

Harlan, J.R., J.M.J. de Wet, K.M. Rawal, M.R. Felder, and W.L. Richardson. 1970a. Cytogenetic studies in *Cynodon* L.C. Rich. (Gramineae). Crop Sci. 10:288-291.

Harlan, J.R., J.M.J. de Wet, W.W. Huffine, and J.R. Deakin. 1970b. A guide to the species of *Cynodon* (Gramineae). Bulletin B-673. Oklahoma State University Experiment Station.

Harlan, J.R., J.M.J. de Wet, and K.M. Rawal. 1970c. Geographic distribution of the species of *Cynodon* L. C. Rich (Gramineae). East African Agricultural and Forestry Journal. 36:220-226.

Harlan, J.R., J.M.J. de Wet, W.R. Richardson, W.W. Huffine, J. Deakin, S.P. Sen Gupta, and A. Carpena. 1966. Biosystematics of the genus Cynodon (Gramineae). Progress Report. Oklahoma State University Experiment Station.

Hartl, D.L. 1991. Basic Genetics, 2nd ed. Jones and Bartlett Publishers, Inc. Boston, MA.

Holland, J.B., and G.P. Munkvold. 2001. Genetic relationships of crown rust resistance, grain yield, test weight, and seed weight in oat. Crop Sci. 41:1041-1050.

Hurcombe, R. 1947. A cytological and morphological study of cultivated *Cynodon* species. J. So. Afr. Bot. 13:107-116.

Johnson, L.D., J.J. Marques-Ortiz, D.K. Barnes, and J.F.S. Lamb. 1996. Inheritance of root traits in alfalfa. Crop Sci. 36:1482-1487.

Juska, F.V., and A.A. Hanson, 1964. Evaluation of bermudagrass varieties for general-purpose turf. Dep. Agric., Agric. Res. Ser., Agric. Handbook no. 270. U.S. Gov. Print. Office, Washington, DC.

Krans, J.V., H.W. Philley, J.M. Goatley, Jr., and V.L. Maddox. 1999. Registration of 'MS-Supreme' bermudagrass. Crop Sci. 39:287.

Lush, J.L. 1945. Animal breeding plans. Iowa State University Press, Ames, IA.

Ortiz, R., and A. Golmirzaie. 2002. Hierarchical and factorial mating designs for quantitative genetic analysis in tetrasomic potato. Theor Appl Genet. 104:675-679.

Powell, J.B., G.W. Burton, and C.M. Taliaferro. 1968. A hexaploid clone from a tetraploid X diploid cross in *Cynodon*. Crop Sci. 8:184-185.

Pixley, K.V., and K.J. Frey. 1991. Combining ability for test weight and agronomic traits of oat. Crop Sci. 31:1448-1450.

Royal Botanic Gardens, Kew. 1999. World grasses database. Published on the internet; http://www.rbgkew.org.uk/herbarium/gramineae/wrldgr.htm (accessed Dec. 22, 2001).

Taliaferro, C.M. 1992. Out of Africa – A new look at "African" bermudagrass. U.S. Golf Assoc. Green Section Record. 30:10-12.

Taliaferro, C.M. 1995. Diversity and vulnerability of Bermuda turfgrass species. Crop Sci. 35:327-332.

Taliaferro, C.M. 2003. Bermudagrass. *In* M.D. Casler, and R.R. Duncan (ed). Turfgrass Biology, Genetics, and Cytotaxonomy. Sleeping Bear Press

Wofford, D.S., and A.A. Baltensperger. 1985. Heritability estimates for turfgrass characteristics in bermudagrass. Crop Sci. 25:133-136.

CHAPTER II

QUANTIFICATION OF THE GENETIC VARIATION IN AFRICAN BERMUDAGRASS (*Cynodon transvaalensis)* FOR PLANT AND INFLORESCENCE MORPHOLOGY

Abstract

The extent of genetic variation in populations of African bermudagrass (*Cynodon transvaalensis*, Burtt-Davy) is not known. In order to quantify the genetic variation for traits in African bermudagrass a Design II mating system was used to develop a genetic population. Traits analyzed in this study were stolon length; numbers of nodes and internodes; stem diameter; internode length; leaf length and width; greenhouse and field plant heights; raceme length; numbers of racemes, florets, and seed per inflorescence; and percent seed set. Families were significantly different for most traits studied. For these traits significant differences were also found regarding additive and non-additive genetic effects. Variance estimates associated with dominance (non-additive) effects were typically of a higher magnitude than variance estimates for males and females (additive effects). Calculated heritability estimates ranged from moderate to high, indicating that breeding and selection methods for improvement of African bermudagrass should be utilized to capitalize on the presence of non-additive genetic effects.

Introduction

There are nine bermudagrass species within the genus, *Cynodon*. Interspecific, triploid, hybrids between *C. dactylon* (L.) Pers. var. *dactylon* (common bermudagrass) and *C. transvaalensis* Burtt-Davy (African bermudagrass) are very important to the turfgrass industry. The importance of the triploid hybrids arose through the work of Dr. Glenn Burton at the University of Georgia Coastal Plain Experiment Station, Tifton, Georgia in the 1950's and 60's. Dr. Burton was the first to make controlled crosses between *C. dactylon* var. *dactylon* and *C. transvaalensis* in an attempt to produce superior turf type bermudagrass plants. The hybrids released from this program are the most important and widely used turfgrasses throughout the warmer climatic regions of the world (Burton, 1973; Burton, 1977; Burton, 1991). The widespread use of relatively few clonally propagated hybrid cultivars has resulted in an increased susceptibility to damage from the possible occurrence of new pests. This problem is further compounded because many widely used cultivars are the result of naturally occurring or man-induced mutations from previously released material (Taliaferro, 1995; Burton, 1973; Burton, 1977; Hanna, 1986; Burton, 1991; Alderson and Sharp, 1993; Hanna, 1996; Hanna and Elsner, 1999; Beard, 2000). The reduction of this risk can best be achieved through the development of new hybrid cultivars representing a broader genetic base. This will require extensive knowledge of available germplasm in order to select parents with desirable characteristics (Taliaferro, 1995).

Genetic variation in common bermudagrass, a tetraploid (2n = 4x = 36), has been well documented with respect to growth habits that range from very small, fine turf types to more robust forage types (Harlan et al., 1970b; Harlan and de Wet, 1969). Harlan and de Wet (1969) stated that morphological variation within the var. *dactylon* is enormous. Baltensperger and colleagues estimated the heritability of selected traits in *C. dactylon* var. *dactylon*, documenting the enormous amount of variation and demonstrating the potential for improvement of these traits through conventional breeding methods (Wofford and Baltensperger, 1985; Coffey and Baltensperger, 1989; Cluff and Baltensperger, 1991).

In contrast, little is known regarding the degree of genetic variation in *C. transvaalensis* (Taliaferro, 1995), a diploid (2n = 2x = 18) indigenous to the Transvaal region of South Africa. Plants are typically described morphologically as being very uniform, small, narrow leaved, and yellow-green in color (Harlan et al., 1970a; Harlan et al., 1970b; de Wet and Harlan, 1971). However, Taliaferro (1992) and Gerken (1994) observed and documented variation for morphological and adaptation traits in segregating populations of *C. transvaalensis*. Taliaferro (1992) screened plants of African bermudagrass for tolerance to putting green conditions and observed variation related to establishment, winter survivability, texture, density, color, and mowing height tolerances. Gerken (1994) noted significant differences for establishment, clipping yield, leaf blade angles, root mass, shoot density, visual density, spring greenup, stimpmeter readings, color,

and turf quality of six accessions of C. transvaalensis along with 'Tifgreen' hybrid bermudagrass and 'Uganda' African bermudagrass.

Information related to phenotypic variation as a result of genetic and environmental components is essential for the plant breeder to make decisions regarding the use of resources and the potential for plant improvement (Hallauer and Miranda, 1981). Estimates of genetic variances (additive and nonadditive gene action) and heritabilities are useful to determine the degree of improvement that might be possible through breeding and selection for desired traits (Dudley and Moll, 1969). Taliaferro (1992) explained that if the observed variation for traits in African bermudagrass is heritable, there exists potential for breeding directed at the development of cultivars or elite germplasm to select parents to produce new triploid interspecific hybrid turf-type bermudagrasses. In order to provide breeders with information regarding the extent of available genetic variation and heritability of any desired trait a genetic population must be developed (Ortiz and Golmirzaie, 2002). The objectives of this study were to estimate genetic variances (additive and non-additive gene action) and heritabilities of selected morphological traits of African bermudagrass.

Materials and Methods

The genetic population was created using the Design II breeding method in which 32 parental plants were randomly selected from a reference population under Hardy-Weinberg equilibrium. Table 2.1 contains the *C. transvaalensis* germplasm accessions that were intercrossed to produce the reference population. The selected parental plants were randomly divided into four sets

providing eight plants per set. Within each set, four plants were randomly designated as females and the remaining four designated as males (Table 2.2). In each set, all males were crossed with all females. Therefore, a total of 64 crosses were made, 16 per set. From each individual cross, five progeny were retained creating 64 full-sib families (Figure 2.1). Full-sib African bermudagrass families are heterogenous with individual plants being heterozygous. These intraspecific crosses were made in May and June of 1992 through 1994. Plant morphological traits evaluated included stolon length; number of nodes and internodes; stem diameter; internode length; leaf length and width; and plant heights in the greenhouse and field. Inflorescence characteristics studied included the number of racemes per inflorescence, raceme length, number of florets per raceme, number of seed per raceme, and percent seed set.

Progeny were planted 30 April, 1996 in a randomized complete block design with three replications at the Agronomy Research Farm, Oklahoma State University, Stillwater, Oklahoma on a Kirkland Silt Loam (fine, mixed, superactive, thermic Udertic Paleustoll). Each set was kept intact in each replication, but the sets were randomly distributed in each replicate block and crosses were randomized within each set. Experimental units were represented by a single cross and are referred to as plots. Each plot consisted of the five F1 progeny plants planted on 1.22 m centers and respectively maintained as 0.5 m^2 plots. The identity of each F1 plant was retained so that inferences could be made back to parents, and replications were planted with clonally propagated material so that each replication contained the same genetic material. In July

Table 2.1. *Cynodon transvaalensis* accessions that contributed to the reference population from which 32 plants were randomly selected as parents.

PI Accessions*	Harlan/Huffine Accessions#			
290874	10140	10154	10210-a	10292
290894	10141	10175	10210-b	10302
290897	10143	10176	10211	10327
290905	10145	10180	10214	10483
291591	10146	10181	10215-a	10493
289922	10147	10188	10216-b	10496
290812	10148	10189	10220	10704
289931	10149	10190	10221	
289922	10151	10197	10290	
286584	10152	10208	10291	

*NPGS (National Plant Germplasm System)
#Harlen et. al., 1966

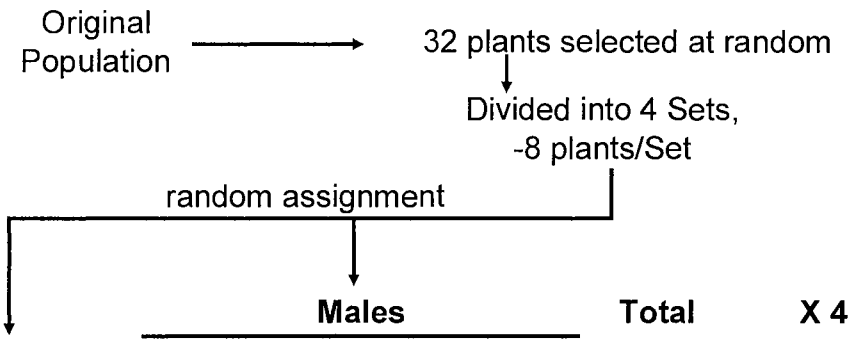
Table 3.2. Thirty-two randomly selected plants used as parents to create a genetic population of *Cynodon transvaalensis.* The plants are divided into their respective sets.

Set 1	Set 2	Set 3	Set 4
F*1 TN 3-6	F1 TN 18-1	F1 TN 30-4	F1 5200 62-4
F2 TN 3-5	F2 TN 18-2	F2 TN 23-3	F2 5200 66-5
F3 TN 3-4	F3 TN 18-3	F3 TN 24-2	F3 5200 67-2
F4 TN 4-3	F4 TN 18-4	F4 TN 25-7	F4 5200 70-2
M#1 TN 17-1	M1 TN 18-5	M1 TN 25-6	M1 5200 72-4
M2 TN 17-2	M2 TN 18-6	M2 TN 27-5	M2 5200 74-6
M3 TN 17-3	M3 TN 19-6	M3 TN 30-7	M3 5200 76-7
M4 TN 17-4	M4 TN 19-4	M4 TN 31-6	M4 5200 80-5

*F = female
#M = male

2001, plugs were taken from the field plots and planted into 10 cm in. diameter, included morphological measurements of stolon length, number of nodes and internodes, stem diameter, internode length, leaf length and width, and plant height. All parameters except plant height were evaluated simultaneously on fully developed plants with many elongated stolons. To begin a trial, plants were trimmed back to the height of the pot, removing all vegetation. To account for the

Figure 2.1. Diagram of the Design II mating scheme used to develop a genetic population of *Cynodon transvaalensis* for evaluation of genetic parameters.



	Males				Total	X 4
Females	M1	M2	M3	M4	**Crosses**	**Sets**
F1	X	X	X	X		
F2	X	X	X	X		
F3	X	X	X	X		
F4	X	X	X	X		
Crosses	4	4	4	4	16	64
5 progeny/cross	20	20	20	20	80	320

length of time required for collecting the morphological data the blocks were staged based on their time of trimming. For example, rep two was trimmed one week after rep one, and rep three, trimmed one week after rep two. For each parameter, three sub-samples were evaluated from each plant. Measurements were repeated in time to account for any variation due to seasonal growth patterns or environmental conditions. Measurements were collected 25 January, 2002 and 14 August, 2002. Stolon length, measured in millimeters (±1.0 mm), was taken by removing three well-elongated stolons at random from the plant. The point where the stolon had grown over the pot served as the break-off point for stolon removal. Stolon length included the area between the break-off point and the end-point where new leaves emerge. Emerging leaves or other mature

leaves often extended beyond this end-point. These leaves were not included in stolon length measurements. The same three stolons were then used for all other morphological measurements.

Number of nodes and internodes were determined by counting along the length of the stolons that were broken off as described above. If a stolon broke within a node, then the numbers of nodes and internodes were equal. If the stolon broke within an internode, then internode counts were one higher than the nodal counts.

Stem diameter was measured in millimeters (± 0. 1 mm) using a caliper. Measurements were taken on the fourth internode from the end of the stolon. Specifically, the measurements were taken just beneath the third node. This prevented the inclusion of sheath material from leaves that were growing out of the fourth node. If the sheaths were too far up the stem, they were pulled back for stem measurement. Also, the stems of *C. transvaalensis* are typically oval shaped; therefore, the stolon was turned so that the thinnest direction was measured. Internode length measurements were made between the third and fourth nodes from the end of the stolon and recorded in millimeters (± 1.0 mm).

Leaf length and width measurements were made on the uppermost, healthy leaf arising from the fourth internode and growing along the stolon. This excluded any leaves growing on secondary stolons out of the fourth node. The leaf to be used had to be growing along the measured stolon and typically its sheath was wrapped around the fourth internode. If the uppermost leaf was necrotic or had senesced, then the next lower leaf was used for measurements.

For measurement, the leaf blade (lamina) was removed from the stolon and leaf sheath and then measured from the base of the blade to its tip. Leaf width measurements were made across the base of the blade. Both traits were measured in millimeters (length = ± 1.0 mm, width = ± 0.1 mm).

Greenhouse plant height measurements were taken on each plant approximately two weeks after trimming. Measurements were made using the top of the pot to represent the base of the plant. Height of the plants in cm (± 0.5 cm) was determined as the height that the majority of the leaves terminated. Data were collected on 13 September, and 16 October 2002.

Data for plant height in the field were also collected twice. In July of 1996, measurements were taken on unmowed plants using a ruler randomly placed within a plant. Plant height in 1996 was recorded in cm (± 1.0 cm). Measurements taken in September of 2002 were collected four days after mowing. The height of each plant was determined using a 7.62 cm diameter piece of PVC pipe 1.22 m in length. One end of the PVC pipe was capped with a small hole drilled in the center for a dowel stick to fit through the cap. The end of the dowel stick protruding through the cap was marked in cm. A lightweight base was attached to the other end of the dowel that was inside the diameter of the pipe. Therefore, as the pipe was placed over the turf, the base and dowel stick were raised. The height in cm (± 0.1 cm) that the dowel stick was raised reflected the height of the underlying turf. Due to the differences in management at the time of measurement the heights determined in 1996 were much higher than those in 2002.

For inflorescence characteristics, mature inflorescences were harvested and placed in coin envelopes during July of 2002 and 2003. Five samples were collected from each plant to gain an accurate representation of the desired characteristics. The number of racemes was counted on each collected inflorescence. Then one raceme from each inflorescence was removed for additional data collection. The length of the removed raceme was measured in millimeters (± 1.0 mm) and the number of spikelets on the raceme counted. To determine the number of seed that were set on the removed raceme, it was placed in a test tube containing a 20% bleach solution for a minimum of 4 hours. Soaking in the bleach caused the palea and lemma to become translucent, revealing the presence or absence of a caryopsis within each spikelet/floret. The five samples were averaged to obtain individual plant averages for the characteristics measured. Percent seed set was then determined by taking the number of spikelets per raceme and multiplying by the number of racemes per inflorescence to get the total number of spikelets possible on an inflorescence. In addition, the number of seed counted per raceme was multiplied by the number of racemes per inflorescence to obtain the total number of seed formed on an inflorescence. These two characteristics were also averaged across the five samples per plant. African bermudagrass is very susceptible to shattering of seed and it should be noted that a significant portion of the spikelets had shattered prior to the analysis of the collected material. This was especially true for the 2002 material. This would not affect the number of spikelets counted per raceme because disarticulation occurs above the glumes. However, it could

significantly affect the number of seed, resulting in an underestimation of the number of seed per inflorescence and a reduced percent seed set. Therefore, the shattered spikelets were collected from each envelope (an envelope represented a plant and its five samples). The numbers of shattered spikelets containing a seed was determined by blowing (2002 material) or by soaking in the 20% bleach solution (2003 material). The additional seed identified among the shattered spikelets was then added to the total seed formed on the five samples already counted and then divided by five to obtain a more accurate average number of seed formed per inflorescence. Taking this number and dividing by the average number of spikelets per inflorescence determined the percent seed set per plant.

Data taken for all traits studied, both field and greenhouse, were analyzed as described by Hallauer and Miranda (1981) for the Design II breeding scheme. Analyses were performed on family means. For data collected over multiple environments an environment refers to a date of evaluation. The analyses over multiple environments determined if significant differences existed for environments (dates) cross/sets males/sets, females/sets, males x females/sets, and cross/environments x sets. A cross represented a family and consisted of the five F1 plants retained to create the genetic population. The analyses were used to provide estimates of the components of genetic variance (additive and dominance effects). Table 2.3 is an illustration of the AOV table used to perform the appropriate tests of significance for the above sources of variation. All sources of variation were considered to be random effects.

Table 2.3. Analysis of variance for the design II: multiple environments.

Source	df	Expected mean squares
Environments (E)	e-1	
Sets (S)	e(s-1)	
S x E	(e-1)(s-1)	
Rep/E	e(r-1)	
Reps (R)/S x E	es(r-1)	
Cross/S	s(mf-1)	$\sigma^2 + r\sigma^2_{ce} + re\sigma^2_{mf} + rem\sigma^2_f + ref\sigma^2_m + re\sigma^2_c$
Males (M)/S	s(m-1)	$\sigma^2 + r\sigma^2_{ce} + re\sigma^2_{mf} + ref\sigma^2_m$
Females (F)/S	s(f-1)	$\sigma^2 + r\sigma^2_{ce} + re\sigma^2_{mf} + rem\sigma^2_f$
M*F/S	s(m-1)(f-1)	$\sigma^2 + r\sigma^2_{ce} + re\sigma^2_{mf}$
Cross/E x S	s(m-1)(e-1)	$\sigma^2 + r\sigma^2_{ce}$
Residual Error	es(r-1)(mf-1)	σ^2
Total	esrmf-1	

When the test for crosses within environments x sets was significant, the environments were analyzed separately (Table 2.4). Differences in environments were expected due to the random selection of dates of trait evaluation. Therefore, if significant interactions associated with environments occurred, separate analysis of environments (date) were not discussed unless the information provided was relevant to the date of selectable variation.

Table 2.4. Analysis of variance for the design II: one environment.

Source	df	Expected mean squares
Reps (R)	r-1	
Sets (S)	s-1	
R x S	(r-1)(s-1)	
Cross/S	s(mf-1)	$\sigma^2 + r\sigma^2_{mf} + rf\sigma^2_m + rm\sigma^2_f + r\sigma^2_c$
Males/S	s(m-1)	$\sigma^2 + r\sigma^2_{mf} + rf\sigma^2_m$
Females/S	s(f-1)	$\sigma^2 + r\sigma^2_{mf} + rm\sigma^2_f$
Males*Females/S	s(m-1)(f-1)	$\sigma^2 + r\sigma^2_{mf}$
Residual Error	s(r-1)(mf-1)	σ^2
Total	srmf-1	

Hallauer and Miranda (1981) stated that this analysis provides estimates of genetic variance components that are estimable from covariances of relatives.

Therefore, when F = 0 (no inbreeding in parents), $\sigma^2_m = \sigma^2_f = 1/4\sigma^2_A$ (additive variance component), and $\sigma^2_{mf} = 1/4\sigma^2_D$ (dominance variance component). Estimates of the components of genetic variances can be equated to covariances among relatives if the parents are random members of the genetic population and if experimental errors are independent. Analysis was performed using SAS Proc GLM with a random statement to determine tests of significance (SAS Institute Inc., 1997). Significant differences associated with cross/sets, males/sets, females/sets, and male x females/sets were determined using cross/environments x sets as the error term. Variance estimates were then determined using the appropriate mean squares associated with each F-test. Variance estimates can be equated to the components of genetic variance. Two independent estimates of the additive variance (σ^2_A) can be calculated from the Design II analysis, one for the males [σ^2_{Am} = 4(covariance of males/sets)], and one for the females [σ^2_{Af} = 4(covariance of females/sets)]. The dominance variance is estimated as [σ^2_D = 4(covariance of males*females/sets)]. Obtaining these genetic variance components allowed for the calculation of heritability estimates. Heritability estimates were calculated on a family mean basis using the variance associated with crosses within sets as the numerator and the mean square of crosses within sets divided by reps*environments as the denominator for traits analyzed over multiple environments. For traits evaluated only once the heritability denominator was determined by dividing the crosses within sets mean square by the number of replications. Heritability estimates were designated as low (0.0 to 0.25), moderate (0.26 to 0.55), or high (0.56 to 0.99).

A. Family-mean heritability, multiple environments:

$$H^2 = \frac{\sigma^2_{cs}}{(\sigma^2 + r\sigma^2_{ces} + re\sigma^2_{cs})/re} = \frac{\sigma^2_{cs}}{\text{ms of crosses/sets} \div re}$$

B. Family-mean heritability, one environments:

$$H^2 = \frac{\sigma^2_{cs}}{(\sigma^2 + r\sigma^2_{ces} + re\sigma^2_{cs})/r} = \frac{\sigma^2_{cs}}{\text{ms of crosses/sets} \div r}$$

Results and Discussion

Plant Morphological Characteristics

Data from the analyses of family plot means of plant morphological data collected in the greenhouse are given in Table 2.5. Crosses within sets were not significantly different ($P>0.05$) for number of nodes, stem diameter, and leaf width indicating a lack of genetic variation. Crosses within sets were significantly different for stolon length, number of internodes, internode length, and leaf length ($P\leq0.01$). The interaction associated with crosses within environments x sets was significant ($P\leq0.05$) for stolon length. This significant interaction was due to changes in rank among family means between the two dates of data collection.

Effects due to males within sets, females within sets, and the males x females within sets interaction were then considered for traits exhibiting significant family differences. Differences associated with males within sets were significant ($P\leq0.01$) for stolon length and number of internodes, while differences attributable to females within sets were significant for number of internodes

Table 2.5. Estimated variance components, heritability estimates, and averages for morphological traits evaluated over two environments.

	Trait						
	Stolon Length	Nodes	Inter-nodes	Stem Diameter	Internode Length	Leaf Length	Leaf Width
Source	----------Variance Estimates----------						
Env. (E)	56.26	3.64**	3.55**	0.01**	32.97**	4.84	0.00
Set (S)	69.00	0.11	0.11	0.00	0.75	2.07	0.00
Crosses/S	243.00**	0.07	0.13**	0.00	4.55**	14.19**	0.00
Male (M)/S	59.25**	NA	0.04**	NA	0.21	1.80	NA
Female (F)/S	29.88	NA	0.04**	NA	0.78*	4.01**	NA
M*F/S	286.24**	NA	0.13**	NA	6.27**	15.80**	NA
Crosses/E x S	106.00*	0.00	0.00	0.00	0.00	1.16	0.00
Residual	609.00	1.04	0.52	0.00	14.71	52.71	0.56
H^2	0.62	NA	0.67	NA	0.67	0.57	NA
Average	268.0 mm	9.0	9.5	0.64 mm	33.0 mm	30.0 mm	1.7 mm

*Differences were significant (P≤0.05)

**Differences were significant (P≤0.01)

(P≤0.01), internode length (P≤0.05), and leaf length (P≤0.01). Interactions of males x females within sets were significant (P≤0.01) for these four traits. Results indicate that the genetic variance of these four traits is comprised of both additive and dominance components, the latter being much greater than the former as indicated by the magnitudes of the variance estimates.

Calculated heritability estimates were moderate (0.57) for leaf length, and high (0.62 to 0.67) for stolon length, number of internodes and internode length (Table 2.5). These moderate to high family mean heritability estimates suggest that selection for changes to these respective traits based on family means should be successful.

Plant Height

There was a significant cross within environment x sets interaction for the field plant height data (Table 2.6). This interaction appears to be due more to a change in magnitude (data not shown) as indicated by the 1996 and 2002 plant height averages which were13.44 cm and 5.43 cm respectively. In 1996, plant heights were measured on fully mature, un-mowed, plants. In contrast, the 2002 measurements were taken on plants that had been maintained through regular mowings with the last mowing occurring four days prior to data collection. Because there was not a significant environment interaction for greenhouse plant heights and the significant interaction for field height was due to a change in magnitude of family means the analysis across environments was used for both data sets. Crosses within sets were not significantly different (P>0.05) for field

2.6. Estimated variance components, heritability estimates, and averages for greenhouse and field plant height measurements evaluated over two environments.

	Plant Height	
	Field	Greenhouse
Source	--Variance Estimates--	
Env. (E)	31.95**	6.33**
Set (S)	0.05	0.19**
Cross/S	0.30	0.26**
Male (M)/S	NA	0.08**
Female (F)/S	NA	0.02*
M*F/S	NA	0.30**
Cross/E x S	0.86**	0.00
Residual	1.25	0.56
H^2	NA	0.75
Average	9.43 cm	7.62 cm

*Differences were significant (P≤0.05)
**Differences were significant (P≤0.01)

heights, but there were significant differences (P≤0.01) for greenhouse heights. Therefore, effects of males within sets, females within sets, and their interaction were analyzed for greenhouse heights. Due to the lack of available genetic variation with respect to field heights no further analysis was performed.

Significant effects were found for males (P≤0.01), females (P≤0.05), and their interaction (P≤0.01) for greenhouse plant heights. The additive variance estimates for males and females are much lower than the variance estimate for the interaction of males and females, indicating that non-additive effects have a greater influence on plant heights as measured in the greenhouse. The heritability estimate for greenhouse plant height was high (0.75), indicating a probable favorable response to selection on the basis of family means.

Inflorescence Characteristics

None of the interactions associated with cross within environments x sets was significant ($P>0.05$) for any of the inflorescence parameters evaluated in the study (Table 2.7). Therefore, analyses were performed across environments. Family means (crosses within sets) were significantly different ($P\leq0.05$) for all inflorescence characteristics; therefore, effects of males within sets, females within sets, and their interaction were determined. Significant effects attributable to males occurred for raceme number ($P\leq0.01$), raceme length ($P\leq0.01$) and the number of florets per inflorescence ($P\leq0.05$). Effects due to females were highly significant ($P\leq0.01$) for all inflorescence traits. Significant ($P\leq0.01$) interactions for male x female within sets were found for raceme number, raceme length, and floret number.

Variance component estimates for raceme number were very low (0.0 to 0.01) suggesting lesser variation for this trait than for the other traits having relatively much higher estimates. For raceme number, the estimate of additive variance based on female parents and the estimate of dominance variance based on the male x female interaction were the same (0.003), while the additive variance estimate based on male parents was 0.001. Dominance variance estimates were higher than additive variances for raceme length, and the number of florets and seed per inflorescence indicating that dominance genetic effects are more important for these traits. The female additive variance estimate was higher than the dominance variance estimate for percent seed set indicating the importance of additive genetic effects for this trait.

Table 2.7. Estimated variance components, heritability estimates, and averages for inflorescence characteristics evaluated over two environments.

	Inflorescence Characteristics				
	Raceme Number	Raceme Length	Floret Number	Seed Number	Percent Seed Set
Source	----------Variance Estimates----------				
Env. (E)	0.002*	0.94**	92.50**	17.35**	339.66**
Set (S)	0.001	0.09*	0.14	0.71	5.65*
Cross/S	0.005**	0.66**	1.57**	0.64*	8.05*
Male (M)/S	0.001**	0.17**	0.31*	0.12	1.17
Female (F)/S	0.003**	0.11**	0.63**	0.33**	5.38**
M*F/S	0.003**	0.73**	1.37**	0.48	4.69
Cross/E x S	0.00	0.01	0.27	0.05	0.05
Residual	0.01	0.80	4.67	4.95	67.23
H^2	0.75	0.83	0.63	0.43	0.42
Average	2.2	19.0 mm	27.0	7.0	26.5%

*Differences were significant (P≤0.05)
**Differences were significant (P≤0.01)

Calculated heritability estimates were moderate (0.42 to 0.43) for the number of seed per inflorescence, and percent seed set, and high (0.63 to 0.83) for raceme number, raceme length, and the number of florets per inflorescence (Table 2.7). Inflorescence characteristics of African bermudagrass should respond well to family mean based selection.

Conclusions

Significant differences were found among families for most traits studied in African bermudagrass. For these traits, significant differences were attributable to males, females, and their interaction, indicating the presence of both additive and dominance genetic effects controlling the inheritance of stolon length, number of internodes, internode length, leaf length, greenhouse plant height,

raceme number, raceme length, floret number, seed number, and percent seed set.

Variance component estimates associated with the male x female interaction were of a magnitude higher than those estimates associated with males or females for all traits except raceme number, and percent seed set. Therefore, for most traits evaluated the major component of the genetic variation in the population was indicated as that due to dominance derived from intra-allelic gene action. This is not surprising considering the degree of heterozygosity that exists for African bermudagrass.

The family-mean heritability estimates are broad-sense because they reflect both additive and non-additive genetic effects that resulted in the differences found among cloned plants. Moderate and high broad-sense heritablility estimates and the presence of non-additive genetic effects as indicated by the higher variance estimates for the male x female interaction may justify the use of a hybrid breeding program for trait improvement in African bermudagrass.

Literature Cited

Alderson, J., and W.C. Sharp. 1993. Grass varieties in the United States, 2ed. U.S. Dep. Agric., Agric. Res. Ser., Agric. Handbook no. 170. U.S. Gov. Print. Office, Washington, DC.

Beard, J.B. 2000. The new high density bentgrass and bermudagrass cultivars for very closely mowed putting greens. Club Managers Assoc. of America 73rd Annual Conference, Atlanta, GA. 193-207.

Burton, G.W. 1973. Breeding bermudagrass for turf. p. 18-22. *In* E.C. Roberts (ed.). Proc. 2nd Int. Turfgrass Res. Conf. Intl. Turfgrass Soc., Blacksburg, VA.

Burton, G.W. 1977. Better turf means better golf: the bermudagrass- past, present, and future. U.S. Golf Assoc. Green Section Record. March:5-7.

Burton, G.W. 1991. A history of turf research at Tifton. U.S. Golf Assoc. Green Section Record. 29(3):12-14.

Cluff, G.J., and A.A. Baltensperger. 1991. Heritability estimates for seed yield and seed yield components in bermudagrass. New Mexico Agric. Exp. Stn. Bull. 759.

Coffey, B.N., and A.A. Baltensperger. 1989. Heritability estimates for selected turfgrass characteristics of bermudagrass evaluated under shade. p. 117-119. *In* H. Takatoh (ed.). Proc. Int. Turfgrass Res. Conf., 6th, 31 July – 5 Aug. 1989, Tokyo, Jpn. Intl. Turfgrass Soc. and Jpn Soc. Turfgrass Sci., Tokyo.

de Wet, J.M.J., and J.R. Harlan. 1971. South African species of *Cynodon* (Gramineae). J. S. Afr. Bot. 37(1):53-56.

Dudley, J.W., and R.H. Moll. 1969. Interpretation and use of estimates of heritability and genetic variances in plant breeding. Crop Sci. 9:257-262.

Gerken, D.A. 1994. Evaluation of African bermudagrass as a putting surface. M.S. Thesis. Dept. Horticulture and Landscape Architecture, Oklahoma State University, Stillwater, OK.

Hallauer, A.R., and J.B. Miranda, Fo., 1981. Quantitative genetics in maize breeding. Iowa State Univ. Press, Ames, IA.

Hanna, W.W. 1986. A bermudagrass Primer and the Tifton bermudagrass. U.S. Golf Assoc. Green Section Record. Jan./Feb.:11-13.

Hanna, W.W. 1996. TW-72: A potential new bermudagrass for golf greens. U.S. Golf Assoc. Green Section Record. Sept./Oct.:11-12.

Hanna, W.W., and J.E. Elsner. 1999. Registration of 'Tifeagle' bermudagrass. Crop Sci. 39:1258.

Harlan, J.R., and J.M.J. de Wet. 1969. Sources of variation in *Cynodon dactylon* (L). Pers. Crop Sci. 9:774-778.

Harlan, J.R., J.M.J. de Wet, W.W. Huffine, and J.R. Deakin. 1970a. A guide to the species of *Cynodon* (Gramineae). Bulletin B-673. Oklahoma State University Experiment Station.

Harlan, J.R., J.M.J. de Wet, and K.M. Rawal. 1970b. Geographic distribution of the species of *Cynodon* L. C. Rich (Gramineae). East African Agricultural and Forestry Journal. 36:220-226.

Ortiz, R., and A. Golmirzaie. 2002. Hierarchical and factorial mating designs for quantitative genetic analysis in tetrasomic potato. Theor Appl Genet. 104:675-679.

SAS institute Inc. 1997. SAS/STAT software: Changes and enhancements through release 6.12. SAS Institute, Inc., Cary, N.C.

Taliaferro, C.M. 1992. Out of Africa – A new look at "African" bermudagrass. U.S. Golf Assoc. Green Section Record. 30:10-12.

Taliaferro, C.M. 1995. Diversity and vulnerability of Bermuda turfgrass species. Crop Sci. 35:327-332.

Taliaferro, C.M. 2003. Bermudagrass. p. 235-256. *In* M.D. Casler, and R.R. Duncan (ed). Turfgrass Biology, Genetics, and Cytotaxonomy. Sleeping Bear Press.

Wofford, D.S., and A.A. Baltensperger. 1985. Heritability estimates for turfgrass characteristics in bermudagrass. Crop Sci. 25:133-136.

CHAPTER III

QUANTIFICATION OF THE GENETIC VARIATION IN AFRICAN BERMUDAGRASS (*Cynodon transvaalensis)* FOR TURFGRASS PERFORMANCE CHARACTERISTICS

Abstract

Little information is available concerning the degree of genetic variation present in African bermudagrass (*Cynodon transvaalensis,* Burtt-Davy). In order to determine the extent of genetic variation in African bermudagrass a Design II mating system was used to develop a genetic population. Characteristics evaluated were: visually-rated and sensor-rated color, density, turf quality, spring greenup, fall dormancy, percent living cover, percent winter kill, inflorescence density and color, average daily growth, plant diameter, and plant biomass. There were significant differences ($P<0.05$ or 0.01) among families for most of the traits. Variance component estimates indicated these differences to be attributable both to additive and non-additive genetic effects. Dominance variance estimates were typically higher than additive variance estimates indicating their greater importance relative to the total genetic variance. Family-mean heritability estimates ranged from moderate to high indicating that selection should be successful in modifying these traits.

Introduction

Information regarding the extent of genetic variation for African bermudagrass (*Cynodon transvaalensis*) is lacking (Taliaferro, 1995). *Cynodon transvaalensis* is a diploid bermudagrass species indigenous to the Transvaal region of South Africa. Plants are typically described as being uniform with small, narrow, yellow-green leaves (Harlan et al., 1970a; Harlan et al., 1970c); de Wet and Harlan, 1971).

The importance of *C. tra*nsvaalensis is related to the development of sterile, triploid, interspecific hybrids created through crosses with common bermudagrass (*C. dactylon*). These hybrids have become the most important and widely used turfgrasses throughout the warmer regions of the world (Burton, 1973; Burton, 1977; Burton 1991). However, the widespread use of only a few cultivars sharing a common genetic background increases the vulnerability of the marketed cultivars to severe injury from strains of pests that might arise (Taliaferro, 1995).

Information related to the genetic variation associated with common bermudagrass is readily available (Wofford and Baltensperger, 1985; Coffey and Baltensperger, 1989; Cluff and Baltensperger, 1991). Taliaferro (1992) and Gerken (1994) observed and documented variation in African bermudagrass for rate of establishment, winter survivability, texture, density, color, mowing heights, clipping yield, leaf blade angles, root mass, spring greenup, stimpmeter readings, and turf quality. If variation associated with these or other traits could be quantified with respect to the extent and kinds of genetic variation, it could be

used in conjunction with information related to common bermudagrass to develop new hybrids with different genetic backgrounds from those currently available.

Phenotypic variation is a result of genetic and environmental components of variance (Hallauer and Miranda, 1981). Estimates of genetic variances (additive and nonadditive gene action) and heritabilities are useful to determine the degree of improvement that might be possible through breeding and selection for desired traits (Dudley and Moll, 1969). Taliaferro (1992) explained that if the observed variation for traits in African bermudagrass is heritable, there exists potential for breeding new sterile, site-specific, hybrid turf-type bermudagrasses, and the development of elite germplasm. Quantification of genetic variation requires the development of a genetic population (Ortiz and Golmirzaie, 2002). The following experiment utilized a genetic population developed following the design II mating scheme to estimate and determine the importance of genetic variances (additive and non-additive gene action) and heritability of traits related to turf performance characteristics of African bermudagrass.

Materials and Methods

The genetic population was created using the Design II breeding method in which 32 parental plants were randomly selected from a reference population under Hardy-Weinberg equilibrium. Table 3.1 contains the *C. transvaalensis* germplasm accessions that were intercrossed to produce the reference population. The selected parental plants were randomly divided into four sets providing eight plants per set. Within each set, four plants were randomly designated as females and the remaining four designated as males (Table 3.2).

Table 3.1. *Cynodon transvaalensis* accessions that contributed to the reference population from which 32 plants were randomly selected as parents.

PI Accessions*	Harlan/Huffine Accessions#			
290874	10140	10154	10210-a	10292
290894	10141	10175	10210-b	10302
290897	10143	10176	10211	10327
290905	10145	10180	10214	10483
291591	10146	10181	10215-a	10493
289922	10147	10188	10216-b	10496
290812	10148	10189	10220	10704
289931	10149	10190	10221	
289922	10151	10197	10290	
286584	10152	10208	10291	

*NPGS (National Plant Germplasm System)
#Harlen et al., 1966

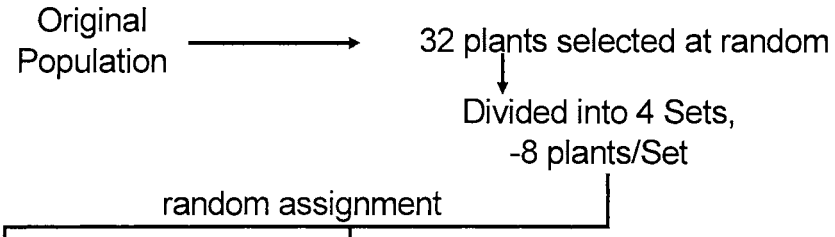
Table 3.2. Thirty-two randomly selected plants used as parents to create a genetic population of *Cynodon transvaalensis.* The plants are divided into their respective sets.

Set 1	Set 2	Set 3	Set 4
F*1 TN 3-6	F1 TN 18-1	F1 TN 30-4	F1 5200 62-4
F2 TN 3-5	F2 TN 18-2	F2 TN 23-3	F2 5200 66-5
F3 TN 3-4	F3 TN 18-3	F3 TN 24-2	F3 5200 67-2
F4 TN 4-3	F4 TN 18-4	F4 TN 25-7	F4 5200 70-2
M#1 TN 17-1	M1 TN 18-5	M1 TN 25-6	M1 5200 72-4
M2 TN 17-2	M2 TN 18-6	M2 TN 27-5	M2 5200 74-6
M3 TN 17-3	M3 TN 19-6	M3 TN 30-7	M3 5200 76-7
M4 TN 17-4	M4 TN 19-4	M4 TN 31-6	M4 5200 80-5

*F = female
#M = male

In each set, all males were crossed with all females. Therefore, a total of 64 crosses were made, 16 per set. From each individual cross, five progeny were randomly selected and retained for a total of 320 plants (Figure 3.1). These intraspecific crosses were made in May and June of 1992. Turfgrass performance traits evaluated included visual ratings for turf density; color; spring green-up; fall dormancy; turf quality; flower color; flower density; percent living

Figure 3.1. Diagram of the design II mating scheme used to develop a genetic population of *Cynodon transvaalensis* for evaluation of genetic parameters.



	Males				Total	X 4
Females	M1	M2	M3	M4	**Crosses**	**Sets**
F1	X	X	X	X		
F2	X	X	X	X		
F3	X	X	X	X		
F4	X	X	X	X		
Crosses	4	4	4	4	16	64
5 progeny/cross	20	20	20	20	80	320

cover; percent winter kill; visual growth habit; and measurements for sensor-rated color, average daily growth rate, plant diameters, and biomass production.

Progeny were planted 30 April, 1996 in a randomized complete block design with three replications at the Agronomy Research Farm, Oklahoma State University, Stillwater, Oklahoma on a Kirkland Silt Loam (fine, mixed,superactive, thermic Udertic Paleustoll). Each set was kept intact in each replication, but the sets were randomly distributed in each replicate block and crosses were randomized within each set. Experimental units are represented by a single cross and are referred to as plots. Each plot consisted of the five F1 progeny

plants planted on 1.22 m centers and respectively maintained as 0.5 m^2 plots. The identity of each F1 plant was retained so that inferences could be made back to parents, and replications were planted with clonally propagated material so that each replication contained the same genetic material.

Visual ratings followed the guidelines of the National Turfgrass Evaluation Program (NTEP) (Morris and Shearman, 2004). Visual ratings for color, density, spring green-up, fall dormancy, turf quality, and inflorescence color and density were based on a one to nine scale (± 1.0), where one rated an entry as a very poor performer and nine as an outstanding entry. Color ratings reflected the inherent color of the genotype, and did not take into account any chlorosis or browning from necrosis. Density was a visual estimate of living plants per unit area or the number of inflorescence per unit area. Dead areas within a plant were ignored for density ratings. Spring green-up was a measure of the transition from winter dormancy to active spring growth. Fall dormancy or color retention was a measure of overall plant color and was used to assess the ability of a genotype to hold color in response to temperature changes or frost occurrences during the fall. Turf quality reflected the aesthetic and functional value of a turf, and was a combination of color, density, uniformity, texture, and damage due to stress. With respect to inflorescence color, a rating of 1 indicated white flowers while numbers greater than one equated to progressively darker colors. A nine flower color rating reflected dark purple flowers. Percent winter kill was based on a percentage (0 to 99; ± 1%) of the plot coverage that failed to generate new growth following winter. Percent living cover is a visual estimate of

the percentage (0 to 99; ± 1%) of live tissue in a plot at any time during active growth. Turf quality and density were rated five times during 2002 and 2003. Color, percent living cover, and percent winter kill were rated twice during 2002 and 2003. Spring greenup was evaluated five times per year for 2002 and 2003. Fall dormancy was rated four times per year during the fall of 2002 and 2003. Inflorescence color and density were each rated once during 2003.

Growth habit ratings were performed to determine if differences could be detected visually between accessions that appeared to be growing upright versus those that have a more prostrate growth habit. Growth habits were evaluated on a scale of 1 to 3, where 1, 2, and 3 designate prostrate, intermediate, and upright growth habits, respectively. Growth habits were evaluated once during 2002.

Sensor-rated color was evaluated using a hand-held optical sensing device developed at Oklahoma State University. The sensor measures irradiance reflected from a turfgrass stand. Red and near infrared (NIR) reflectance can be collected from sensors and converted to normalized difference vegetative indices (NDVI). The NDVI number (± 1.0) represents an unknown combination of turf characteristics that are influenced by turf color and percent living cover (PLC). Bell et al. (2002) developed a model that predicts NDVI of tall fescue (*Festuca arundinaceae* Schreb) from visual ratings for turf color and PLC ($NDVI = 0.258 + 0.4867*\log_{10}$ turf color $+ 1.053 \times 10^{-7}*PLC^3$, $R^2 = 0.80$). Turf color was rated on a 1 to 9 scale and PLC on a 0 to 99 scale. The NDVI can be used to estimate either turf color or PLC by measuring one and solving for the other. Because percent living cover is easier to visually estimate

than turf color, NDVI is more useful when it is used to determine turf color (Bell et al., 2002).

Before relying on the hand-held sensor to estimate turf color, the tall fescue model was tested to determine if it could be used to estimate turf color of *C. transvaalensis*. Testing the model required that visual ratings be recorded for both turf color and percent living color since these values are used in the model to calculate NDVI. To test the model, the calculated NDVI was correlated with NDVI measurements made with the hand-held sensor. The strength of the correlation determined if the tall fescue model could be used to estimate turf color of *C. transvaalensis*.

After calculating NDVI from visual ratings for turf color and PLC, and collecting NDVI measurements using the hand-held sensor, a correlation coefficient of r = .76 was obtained. Therefore, it was judged possible to use the model developed for tall fescue to estimate turf color of *C. transvaalensis* using the sensor. Determination of color using the sensor occurred twice during 2002.

The average daily growth was measured by taking height measurements immediately after mowing the field plots. Since the field was not uniformly smooth, this measurement provided a base plant height or height of cut for each plant. Subsequent measurements were made daily after mowing until the next mowing period. Daily growth was determined by subtracting the previous day's plant height measurement from the current day's measurement over a period of four days. Each day's daily growth rate was averaged to determine the average daily growth rate. Daily growth or plant height was assessed by taking one

random sample from each plant using a 7.6 cm piece of PVC pipe 1.2 m in length. One end of the PVC pipe was capped with a small hole drilled in the center for a dowel stick to fit through the cap. The end of the dowel stick protruding through the cap was marked in centimeters. A lightweight base was attached on the other end of the dowel inside the diameter of the pipe. Therefore, as the pipe was placed over the turf, the base and dowel stick were raised. The number of centimeters (± 0.1 cm) that the dowel stick was raised reflected the height of the underlying turf. Average daily growth rate was determined once during 2002.

The plant diameters represented the average circular spread of a given plant. These data, collected in 1996, were measured in centimeters (± 0.1 cm). Plant biomass collected in 1996 was determined by placing a quadrant over a fully developed, mature plant of African bermudagrass and harvesting the entire quadrant. Both fresh and dry weights measured in grams (± 0.01 gm) were recorded for the harvested plant material. The majority of quadrants harvested were 30 x 30 cm; however, for reasons unknown some samples were collected from different size quadrants or an entire plant was harvested. Information was retained regarding the size of the harvested area for each plant. In order to equate all samples the biomass data was equilibrated to kilograms per hectare (± 1.0 kg).

Data taken for all traits were analyzed as described by Hallauer and Miranda (1981) for the Design II breeding scheme. Analyses were performed on family means. For data collected over multiple environments an environment

refers to a date of evaluation. The analyses over multiple environments determined if significant differences existed for environments (dates) crosses/sets males/sets, females/sets, males x females/sets, and crosses/environments x sets. A cross represented a family and consisted of the five F1 plants retained to create the genetic population. The analyses were used to provide estimates of the components of genetic variance (additive and dominance effects). Table 3.3 is an illustration of the AOV table used to perform the appropriate tests of significance for the above sources of variation. All sources of variation were considered to be random effects.

When the test for crosses within environments x sets was significant, the environments were analyzed separately (Table 3.4). Differences in environments were expected due to the random selection of dates of trait evaluation. Therefore, if significant interactions associated with environments occurred, separate analysis of environments (date) were not discussed unless the information provided was relevant to the date of selectable variation. This analysis was also used for traits that were evaluated only once.

Table 3.3. Analysis of variance for the design II: multiple environments.

Source	df	Expected mean squares
Environments (E)	e-1	
Sets (S)	e(s-1)	
S x E	(e-1)(s-1)	
Rep/E	e(r-1)	
Reps (R)/S x E	es(r-1)	
Crosses/S	s(mf-1)	$\sigma^2 + r\sigma^2_{ces} + re\sigma^2_{cs}$
Males (M)/S	s(m-1)	$\sigma^2 + r\sigma^2_{ces} + re\sigma^2_{mfs} + ref\sigma^2_{ms}$
Females (F)/S	s(f-1)	$\sigma^2 + r\sigma^2_{ces} + re\sigma^2_{mfs} + rem\sigma^2_{fs}$
M*F/S	s(m-1)(f-1)	$\sigma^2 + r\sigma^2_{ces} + re\sigma^2_{mfs}$
Crosses/E x S	s(m-1)(e-1)	$\sigma^2 + r\sigma^2_{ces}$
Residual Error	es(r-1)(mf-1)	σ^2
Total	esrmf-1	

Table 3.4. Analysis of variance for the design II: one environment.

Source	df	Expected mean squares
Reps (R)	r-1	
Sets (S)	s-1	
R x S	(r-1)(s-1)	
Cross/S	s(mf-1)	$\sigma^2 + + r\sigma^2_{cs}$
Males/S	s(m-1)	$\sigma^2 + r\sigma^2_{mfs} + rf\sigma^2_{ms}$
Females/S	s(f-1)	$\sigma^2 + r\sigma^2_{mfs} + rm\sigma^2_{fs}$
Males*Females/S	s(m-1)(f-1)	$\sigma^2 + r\sigma^2_{mfs}$
Residual Error	s(r-1)(mf-1)	σ^2
Total	srmf-1	

Hallauer and Miranda (1981) stated that this analysis provides estimates of genetic variance components that are estimable from covariances of relatives. Therefore, when F = 0 (no inbreeding in parents), $\sigma^2_m = \sigma^2_f = 1/4\sigma^2_A$ (additive variance component), and $\sigma^2_{mf} = 1/4\sigma^2_D$ (dominance variance component). Estimates of the components of genetic variances can be equated to covariances among relatives if the parents are random members of the genetic population and if experimental errors are independent. Analyses were performed using SAS Proc GLM with a random statement to determine tests of significance (SAS Institute Inc., 1997). Significant differences associated with cross/sets, males/sets, females/sets, and male x females/sets were determined using cross/environments x sets as the error term. Variance estimates were then determined using the appropriate mean squares associated with each F-test. Variance estimates can be equated to the components of genetic variance. Two independent estimates of the additive variance (σ^2_A) can be calculated from the Design II analysis, one for the males [σ^2_{Am} = 4(covariance of males/sets)], and one for the females [σ^2_{Af} = 4(covariance of females/sets)]. The dominance variance is estimated as [σ^2_D = 4(covariance of males*females/sets)]. Heritability

estimates were calculated on a family mean basis using the variance associated with crosses within sets as the numerator and the mean square of crosses within sets divided by reps*environments as the denominator for traits analyzed over multiple environments. For traits evaluated only once the heritability denominator was determined by dividing the crosses within sets mean square by the number of replications.

A. Family-mean heritability, multiple environments:

$$H^2 = \frac{\sigma^2_{cs}}{(\sigma^2 + r\sigma^2_{ces} + re\sigma^2_{cs})/re} = \frac{\sigma^2_{cs}}{\text{ms of crosses/sets} \div re}$$

B. Family-mean heritability, one environment:

$$H^2 = \frac{\sigma^2_{cs}}{(\sigma^2 + r\sigma^2_{ces} + re\sigma^2_{cs})/r} = \frac{\sigma^2_{cs}}{\text{ms of crosses/sets} \div r}$$

Results and Discussion

Multiple Environments

Data from the analyses of family plot means for turgrass performance data evaluated over multiple dates are given in Table 3.5. Crosses within sets were not significantly different ($P>0.05$) for percent winter kill indicating a lack of genetic variation. Crosses within sets were significantly different ($P\leq0.01$) for visual color, density, turf quality, spring green-up, fall dormancy, percent living cover, and sensor color. The interaction of crosses within environments x sets was significant for visual color ($P\leq0.01$), turf quality ($P\leq0.05$), and fall dormancy ($P\leq0.01$). The interaction for visual color was due to a change in magnitude of data responses; therefore, the analysis across environments was appropriate.

Table 3.5. Estimated variance components, heritability estimates, and averages for turfgrass performance traits evaluated over two environments.

	Trait							
	Visual Color	Density	Turf Quality	Spring Green-up	Fall Dormancy	% Living Cover	% Winter Kill	Sensor Color
Source	----------Variance Estimates----------							
Env. (E)	0.12**	0.80**	0.69**	3.63**	3.81**	7.17**	79.70**	1.20**
Set (S)	0.02**	0.00	0.00	0.00	0.01*	0.19	0.00	0.00
Cross/S	0.06**	0.04**	0.03**	0.04**	0.01**	5.36**	2.09	0.10**
Male (M)/S	0.03**	0.01*	0.01**	0.01**	0.01*	2.00**	NA	0.02*
Female (F)/S	0.02**	0.01**	0.01**	0.01**	0.00	0.97**	NA	0.03**
M*F/S	0.02	0.03**	0.03**	0.04**	0.01**	4.97**	NA	0.01**
Cross/E x S	0.02**	0.01	0.02*	0.00	0.08**	0.00	0.78	0.00
Residual	0.18	0.23	0.25	0.21	0.23	14.20	28.46	0.41
H^2	0.59	0.5	NA	0.89	NA	0.92	NA	0.65
Average	6.6	7.0	6.4	6.9	5.2	96.0%	7.00%	9.0

*Differences were significant (P≤0.05).
**Differences were significant (P≤0.01).

Due to the significant interactions for turf quality and fall dormancy, analyses of variance were conducted for individual dates of evaluation according to the single environment analysis of variance shown in Table 3.4.

The effects of males within sets, females within sets, and the male x female within sets interaction were then considered for those traits exhibiting significant family (cross within sets) differences (Table 3.5). Differences attributable to males within sets were significant for visual-rated color ($P \leq 0.01$), density ($P \leq 0.05$), spring green-up ($P \leq 0.01$), percent living cover ($P \leq 0.01$), and sensor-rated color ($P \leq 0.05$). Significant differences ($P \leq 0.01$) for females within sets were found for visual-rated and sensor-rated color, density, spring green-up, and percent living cover. The interactions of males and females within sets were significant ($P \leq 0.01$) for density, spring green-up, percent living cover and sensor color. These results indicate that both additive and dominance components of genetic variance contribute to density, spring green-up, percent living cover, and visually-rated and sensor-rated color. Based on the magnitudes of the estimated variance components the dominance variance associated with the interaction of males and females within sets is more influential than the additive effects of males within sets and females within sets for density, spring green-up, and percent living cover. The opposite was true for visually-rated and sensor-rated color where it appears that the additive effects were equal to, or perhaps slightly greater than, dominance effects.

Calculated heritability estimates were moderate (0.5) for density, and high (0.59 to 0.92) for visually-rated and sensor-rated color, spring green-up, and

percent living cover (Table 3.5). Therefore, family-mean based selection should result in a favorable response for these traits.

Turf Quality

Due to the significant ($P \leq 0.05$; Table 3.5) cross within environments x sets interaction for turf quality the five dates of evaluation were analyzed separately to test the effects of cross within sets, males within sets, females within sets, and the male x female within sets interaction (Table 3.6). For the first, and second dates of turf quality ratings, 27 Apr. 2002, and 21 May 2002 respectively, differences were not significant ($P > 0.05$) for the effect of crosses within sets, indicating that variation in turf quality does not exist during the early part of the growing season. Differences due to crosses within sets were significantly different ($P \leq 0.01$) for the 26 Aug. 2002, 28 Sept. 2003, and 18 Oct. 2003.

Differences attributable to both males and females within sets were significant ($P \leq 0.01$) for 26 Aug. 2002, and 28 Sept. 2003; and not significant ($P > 0.05$) for 18 Oct. 2003. The male x female within sets interactions were significant for all three dates, 26 Aug. 2002 ($P \leq 0.01$), 28 Sept. 2003 ($P \leq 0.01$), and 18 Oct. 2003 ($P \leq 0.05$). These results illustrate that the genetic variance of turf quality is attributable to both additive and dominance components with the dominance variance having the greatest influence as indicated by the magnitudes of the estimated variance components.

Heritability estimates calculated for turf quality were moderate, 0.53 and 0.33, on 28 Sept. 2002 and 18 Oct. 2003 respectively, and high (0.69) on 26 Aug. 2002 (Table 3.6). Results indicate that the degree of variation in turf quality

Table 3.6. Estimated variance components, heritability estimates and averages for turf quality ratings taken in 2002 and 2003.

	Turf Quality				
	4/27/2002	5/21/2002	8/26/2002	9/28/2002	10/18/2003
Source	----------Variance Estimates----------				
Rep	0.02	0.01	0.04	0.05*	0.00
Set (S)	0.00	0.01	0.02	0.03	0.00
Cross/S	0.05	0.01	0.09**	0.08**	0.04**
Male/S	NA	NA	0.02**	0.02**	0.01
Female/S	NA	NA	0.03**	0.02**	0.01
M x F/S	NA	NA	0.09**	0.08**	0.05*
Residual	0.45	0.24	0.12	0.22	0.24
H^2	NA	NA	0.69	0.53	0.33
Averages	6.4	6.6	6.7	7.4	5.0

*Differences were significant (P≤0.05).
**Differences were significant (P≤0.01).

of African bermudagrass fluctuates based on the time of the growing season. Typically, the turf quality of African bermudagrass is very high during the early part of the growing season. As temperatures progressively get hotter through the growing season turf quality will decline. During the end of the growing season, as the heat dissipates, turf quality of African bermudagrass will improve. This trend is illustrated by Table 3.6, which indicates the presence of variation to exist during the period when turf quality declines as a result of increased temperatures. Existence of this variation and the heritability estimates provide hope of selection for improvements in turf quality of African bermudagrass during late summer heat stress.

Fall Dormancy

Fall Dormancy of African bermudagrass evaluated over four dates in 2002 and four dates in 2003 resulted in a significant cross within environments x sets

interaction (Table 3.5). This interaction appears to be related to the differences between the fall of 2002 and the fall of 2003. The fall of 2003 was milder than the fall of 2002. Prior to the last rating in 2002 there had been eight freezing events whereas in 2003 there had been only two freezing events prior to the last rating (Figure 3.2).

Because of this interaction dates were analyzed separately to determine if differences attributable to crosses within sets were significant (Table 3.7). Differences were not significant ($P>0.05$) for the last two dates in 2003, 8 Nov. 2003 and 15 Nov. 2003; however, all other dates did have significant differences ($P\leq0.01$) which warranted further analysis of males, females and males x females within sets. Differences due to males within sets for the first two dates of fall dormancy evaluation during both years were significant: 22 Oct. 2002 ($P\leq0.01$), 31 Oct. 2002 ($P\leq0.01$), 26 Oct. 2003 ($P\leq0.05$), and 2 Nov. 2003 ($P\leq0.01$). Females within sets were significantly different for the first date in 2002 (22 Oct. 2002, $P\leq0.05$), and the first two dates in 2003 (26 Oct. 2003, $P\leq0.01$; and 2 Nov. 2003, $P\leq0.01$). The interactions of males x females within sets were significant ($P\leq0.01$) for all dates of analysis except the first date of fall dormancy evaluation in 2003 ($P>0.05$). Therefore, as indicated by both years, additive effects due to males and females have a greater impact during early fall. Four of eight dates indicate that both additive and dominance effects contribute to the total genetic variance associated with fall dormancy of African bermudagrass. However, most dates, (five out of eight) based on the relative magnitudes of their variance estimates show that fall dormancy is influenced

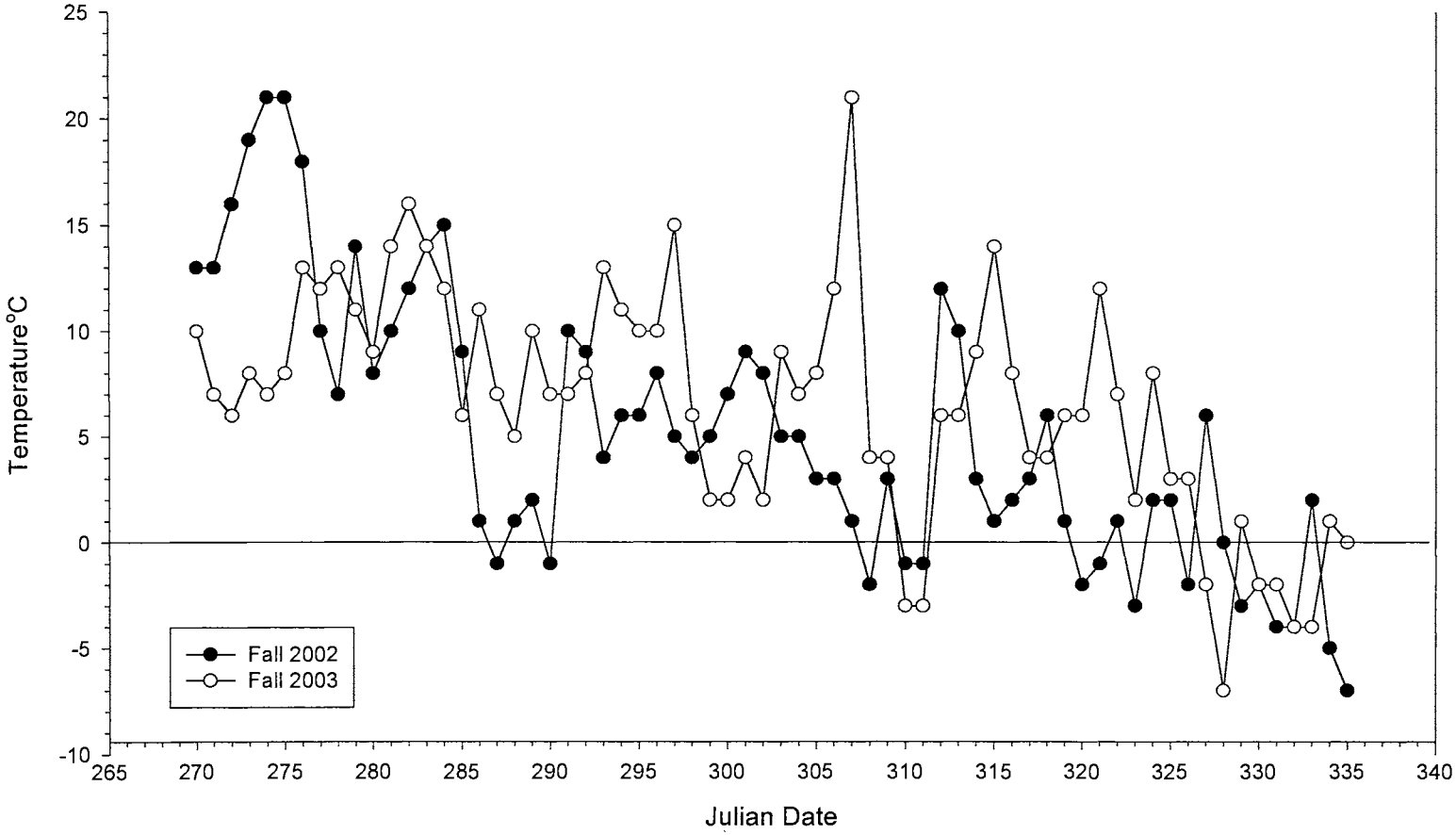


Figure 3.2 Minimum daily temperature Julian Date 270 to 335 (1 Oct. to 1 Dec.) at Stillwater, Oklahoma. Four dates of 2002 fall dormancy ratings: 22 Oct. (295), 25 Oct. (304), 11 Nov. (315), and 21 Nov. (325). Four dates of 2003 fall dormancy ratings: 26 Oct. (299), 2 Nov. (306), 8 Nov. (312), and 15 Nov. (319).

Table 3.7. Estimated variance components, heritability estimates, and averages for fall dormancy ratings taken in 2002 and 2003.

	Fall Dormancy							
	10/22/02	**10/31/02**	**11/11/02**	**11/21/02**	**10/26/03**	**11/2/03**	**11/8/03**	**11/15/03**
Source	**----------Variance Estimates----------**							
Rep	0.00	0.00	0.14**	0.003	0.13**	0.07	0.00	0.00
Set (S)	0.02	0.06	0.01	0.03	0.01	0.02	0.00	0.003
Cross/S	0.27**	0.21**	0.05**	0.04**	0.03**	0.08**	0.03	0.003
Male/S	0.11**	0.08**	0.005	0.003	0.01*	0.03**	NA	NA
Female/S	0.04*	0.02	0.004	0.001	0.02**	0.03**	NA	NA
M x F/S	0.26**	0.22**	0.07**	0.07**	0.01	0.06**	NA	NA
Residual	0.41	0.39	0.17	0.12	0.12	0.13	0.29	0.25
H^2_{bm}#	0.66	0.62	0.49	0.48	0.43	0.62	NA	NA
Averages	6.5	6.0	3.0	2.3	8.2	6.3	4.5	4.5

*Differences were significant (P≤0.05).
**Differences were significant (P≤0.01).

more by dominance effects than additive effects.

Calculated heritability estimates ranged from moderate (0.43 to 0.49) on 11 Nov. 2002, 21 Nov. 2002, and 26 Oct. 2003 to high (0.62 to 0.66) on 22 Oct. 2002, 31 Oct. 2002, and 2 Nov. 2003 (Table 3.7). Therefore, selection of fall dormancy based on family-means should be successful, and according to both years selection should take place in early fall because additive effects are more prominent at this time.

Single Environments

The remaining traits (Table 3.8) were evaluated only once during the experiment; therefore, their respective analyses were as outlined in Table 3.4. Family means were not significantly different ($P>0.05$) for average daily growth or dry weight biomass accumulation, indicating that little genetic variation exists for these two traits. Differences due to family means were significant for inflorescence color and density ($P\leq0.01$), growth habit ($P\leq0.01$), plant diameter ($P\leq0.01$), and fresh weight biomass accumulation ($P\leq0.05$). For these traits subsequent analyses were performed to determine the effects of males within sets, females within sets, and the interaction of males x females within sets. Males within sets were significantly different ($P\leq0.01$) for inflorescence color and density, growth habit, and plant diameter, while differences attributable to females within sets were significant for inflorescence color ($P\leq0.01$), inflorescence density ($P\leq0.05$), growth habit ($P\leq0.01$), and fresh weight biomass ($P\leq0.01$). The interaction of males and females within sets was significant for inflorescence color ($P\leq0.01$), inflorescence density ($P\leq0.05$), growth habit

Table 3.8. Estimated variance components, heritability estimates, and averages for inflorescence, growth, and biomass traits of African bermudagrass.

	Trait						
Source	Inflorescence Color	Inflorescence Density	Growth Habit	Average Daily Growth	Plant Diameter	Fresh Weight Biomass	Dry Weight Biomass
	----------Variance Estimates----------						
Rep	0.02*	0.11**	0.01	0.001	0.00	0.00	0.00
Set (S)	0.01	0.09**	0.02	0.00	0.00	0.00	0.00
Cross/S	0.14**	0.05**	0.07**	0.001	66.63**	852503.00*	125868.00
Male/S	0.03**	0.04**	0.02**	NA	19.81**	9537.00	NA
Female/S	0.05**	0.01*	0.03**	NA	6.24	777380.00**	NA
M x F/S	0.12**	0.03*	0.05**	NA	76.32**	371614.00	NA
Residual	0.14	0.11	0.12	0.003	125.9	5094853.00	1027517.00
H^2	0.77	0.56	0.65	NA	0.61	0.32	NA
Averages	6.8	6.4	2.4	0.25 cm	83.8 cm	9673 kg/ha	4024 kg/ha

*Differences were significant (P≤0.05).
**Differences were significant (P≤0.01).

(P≤0.01), and plant diameter (P≤0.01). These results suggest the presence of both additive and dominance genetic variance for the traits analyzed. Based on the magnitudes of variance estimates the dominance (non-additive) effects had a greater influence on the genetic variance for inflorescence color, growth habit, and plant diameter than additive effects. However, additive effects were more important for inflorescence density and fresh weight biomass.

Heritability of fresh weight biomass was moderate (0.32), estimates were high (0.56 to 0.77) for inflorescence color and density, growth habit, and plant diameter (Table 3.8). Heritabilities for these traits suggest a favorable response to selection if based on family means.

Conclusions

Significant differences were found among families for most of the traits studied in African bermudagrass. Variances associated with males, females, and their interaction indicate that both additive and dominance (non-additive) genetic effects contribute to the observed variation for visually-rated and sensor-rated color, density, turf quality, spring greenup, fall dormancy, percent living cover, inflorescence color and density, growth habit, plant diameter, and wet plant biomass accumulation.

Dominance effects resulting from intra-allelic gene action in African bermudagrass have the greatest impact on the total available genetic variation for most traits studied. This is supported by the higher variance estimates associated with the male x female interaction than the additive estimates for males and females for all traits except visually-rated and sensor-rated color,

inflorescence density, and fresh weight biomass. Considering the extent of heterozygosity that exists for African bermudagrass these results are not surprising.

Since family-mean heritability estimates are the result of differences among cloned plants they are broad-sense estimates because they reflect both additive and non-additive genetic effects. The presence of moderate and high heritability estimates along with the overall genetic variance being attributed to dominance effects may justify the use of a hybrid breeding program for trait improvement in African bermudagrass.

Literature Cited

Bell, G.E., D.L. Martin, S.G. Wiese, D.D. Dobson, M.W. Smith, M.L. Stone, and J.B. Solie. 2002. Vehicle-mounted optical sensing: an objective means for evaluating turf quality. Crop Sci. 42:197-201.

Burton, G.W. 1973. Breeding bermudagrass for turf. p. 18-22. *In* E.C. Roberts (ed.). Proc. 2nd Int. Turfgrass Res. Conf. Intl. Turfgrass Soc., Blacksburg, VA.

Burton, G.W. 1977. Better turf means better golf: the bermudagrass- past, present, and future. U.S. Golf Assoc. Green Section Record. March:5-7.

Burton, G.W. 1991. A history of turf research at Tifton. U.S. Golf Assoc. Green Section Record. 29(3):12-14.

Cluff, G.J., and A.A. Baltensperger. 1991. Heritability estimates for seed yield and seed yield components in bermudagrass. New Mexico Agric. Exp. Stn. Bull. 759.

Coffey, B.N., and A.A. Baltensperger. 1989. Heritability estimates for selected turfgrass characteristics of bermudagrass evaluated under shade. p. 117-119. *In* H. Takatoh (ed.). Proc. Int. Turfgrass Res. Conf., 6th, 31 July – 5 Aug. 1989, Tokyo, Jpn. Intl. Turfgrass Soc. and Jpn Soc. Turfgrass Sci., Tokyo.

de Wet, J.M.J., and J.R. Harlan. 1971. South African species of *Cynodon* (Gramineae). J. S. Afr. Bot. 37(1):53-56.

Dudley, J.W., and R.H. Moll. 1969. Interpretation and use of estimates of heritability and genetic variances in plant breeding. Crop Sci. 9:257-262.

Gerken, D.A. 1994. Evaluation of African bermudagrass as a putting surface. M.S. Thesis. Dept. Horticulture and Landscape Architecture, Oklahoma State University, Stillwater, OK.

Hallauer, A.R., and J.B. Miranda, Fo., 1981. Quantitative genetics in maize breeding. Iowa State Univ. Press, Ames, IA.

Harlan, J.R., J.M.J. de Wet, K.M. Rawal, M.R. Felder, and W.L. Richardson. 1970a. Cytogenetic studies in *Cynodon* L.C. Rich. (Gramineae). Crop Sci. 10:288-291.

Harlan, J.R., J.M.J. de Wet, and K.M. Rawal. 1970b. Geographic distribution of the species of *Cynodon* L. C. Rich (Gramineae). East African Agricultural and Forestry Journal. 36:220-226.

Morris, K.N., and R.C. Shearman. NTEP turfgrass evaluation guidelines. National Turfgrass Evaluation Program. Published on the internet; http://www.ntep.org/pdf/ratings.pdf (accessed 2 May 2004).

Ortiz, R., and A. Golmirzaie. 2002. Hierarchical and factorial mating designs for quantitative genetic analysis in tetrasomic potato. Theor Appl Genet. 104:675-679.

SAS institute Inc. 1997. SAS/STAT software: Changes and enhancements through release 6.12. SAS Institute, Inc., Cary, N.C.

Taliaferro, C.M. 1992. Out of Africa – A new look at "African" bermudagrass. U.S. Golf Assoc. Green Section Record. 30:10-12.

Taliaferro, C.M. 1995. Diversity and vulnerability of Bermuda turfgrass species. Crop Sci. 35:327-332.

Wofford, D.S., and A.A. Baltensperger. 1985. Heritability estimates for turfgrass characteristics in bermudagrass. Crop Sci. 25:133-136.

APPENDIX A

CHAPTER II FAMILY MEANS

Table A.1 Family means for stolon length, number of nodes, number of internodes, stem diameter, internode length, leaf length, and leaf width.

			stolon length	Number of Nodes	Number of Internodes	Stem Diameters	Internode Length	Leaf Length	Leaf Width
Family			Units						
set	male	female	cm				mm	mm	mm
1	1	1	304.92	10.18	10.72	0.64	32.80	21.61	1.62
1	1	2	239.20	8.97	9.62	0.53	27.53	31.42	1.53
1	1	3	323.87	10.01	10.48	0.64	35.14	27.23	1.55
1	1	4	259.10	8.57	9.12	0.45	35.74	37.13	1.73
1	2	1	265.40	10.32	10.79	0.52	28.32	20.49	1.52
1	2	2	278.73	9.13	9.60	0.64	35.29	24.53	1.64
1	2	3	270.18	9.60	10.06	0.56	30.72	27.87	1.61
1	2	4	253.52	8.64	9.13	0.54	31.55	32.44	1.53
1	3	1	297.64	9.66	10.23	0.56	33.63	29.46	1.70
1	3	2	317.04	9.84	10.42	0.57	35.94	41.13	1.80
1	3	3	270.58	9.76	10.36	0.58	29.61	27.48	3.27
1	3	4	292.07	10.29	10.76	0.61	30.16	22.96	1.61
1	4	1	300.76	8.77	9.24	0.55	39.30	37.86	1.84
1	4	2	280.07	9.27	9.84	0.58	30.59	29.82	1.66
1	4	3	270.53	9.99	10.48	0.61	29.74	26.22	1.65
1	4	4	282.19	8.80	9.42	0.54	36.22	27.88	1.73
2	1	1	304.66	9.32	9.98	0.71	36.52	34.10	1.87
2	1	2	284.97	9.01	9.73	0.61	34.32	32.39	1.87
2	1	3	254.11	8.52	9.26	0.55	32.04	30.52	1.77
2	1	4	262.92	8.70	9.36	0.49	33.91	32.05	1.80
2	2	1	279.88	8.92	9.59	0.70	35.08	32.05	1.85
2	2	2	275.74	8.58	9.10	0.49	37.51	32.89	1.85

	Family		stolon length	Number of Nodes	Number of Internodes	Stem Diameters	Internode Length	Leaf Length	Leaf Width
			----------Units----------						
set	male	female	cm				mm	mm	mm
2	2	3	248.98	8.16	8.76	0.52	35.32	34.71	1.75
2	2	4	261.02	8.82	9.50	0.60	33.66	35.24	1.79
2	3	1	257.08	8.44	8.99	0.53	35.18	35.49	1.71
2	3	2	271.73	9.08	9.66	0.55	34.38	24.94	1.65
2	3	3	289.77	8.49	9.19	0.53	36.86	30.04	1.74
2	3	4	242.09	9.01	9.68	0.61	30.82	27.06	1.56
2	4	1	253.28	8.48	9.06	0.53	34.45	36.67	1.84
2	4	2	284.52	8.56	9.12	0.61	38.26	37.65	1.88
2	4	3	252.33	8.31	8.99	0.54	33.43	31.28	1.59
2	4	4	260.53	8.80	9.51	0.60	32.93	32.90	1.85
3	1	1	269.11	8.57	9.19	0.53	33.64	29.44	1.70
3	1	2	260.01	8.30	8.99	0.52	34.85	35.60	1.76
3	1	3	246.54	9.00	9.64	0.54	30.74	24.19	1.65
3	1	4	270.76	8.60	9.13	0.48	35.14	33.87	1.71
3	2	1	241.34	8.49	9.22	0.55	33.41	32.26	1.74
3	2	2	273.39	8.59	9.18	0.61	35.63	31.44	1.66
3	2	3	289.59	9.74	10.39	0.56	31.20	29.11	1.63
3	2	4	246.42	8.88	9.33	0.53	30.13	24.69	1.64
3	3	1	248.79	8.22	8.87	0.52	33.32	33.84	1.62
3	3	2	284.68	8.80	9.39	0.52	35.07	25.08	1.64
3	3	3	263.18	8.78	9.52	0.57	32.00	25.60	1.51
3	3	4	240.99	8.40	9.09	0.49	31.12	30.29	1.64
3	4	1	251.45	9.26	9.87	0.59	28.14	33.46	1.67
3	4	2	251.13	8.81	9.27	0.50	31.78	24.18	1.36

	Family		stolon length	Number of Nodes	Number of Internodes	Stem Diameters	Internode Length	Leaf Length	Leaf Width
			----------Units----------						
set	male	female	cm				mm	mm	mm
3	4	3	265.48	8.46	9.04	0.51	35.20	33.28	2.59
3	4	4	255.44	9.27	9.86	0.49	30.58	21.87	1.58
4	1	1	256.11	8.87	9.39	0.51	30.67	20.87	1.53
4	1	2	257.08	8.50	8.99	0.45	34.69	31.90	1.49
4	1	3	290.00	8.84	9.33	0.49	35.69	31.03	1.67
4	1	4	295.68	8.86	9.34	0.51	36.38	36.31	1.79
4	2	1	263.09	8.19	8.78	0.53	34.87	33.63	1.57
4	2	2	259.76	9.39	9.88	0.52	30.25	20.52	1.43
4	2	3	246.03	8.59	8.94	0.46	32.30	31.55	1.57
4	2	4	278.19	8.88	9.42	0.52	35.45	34.42	1.65
4	3	1	274.27	9.04	9.46	0.52	32.95	31.99	1.73
4	3	2	259.40	8.72	9.24	0.61	31.38	26.13	1.56
4	3	3	278.94	9.36	9.86	0.51	32.91	27.82	1.57
4	3	4	287.59	9.43	9.53	0.48	33.36	27.72	1.80
4	4	1	278.96	8.69	9.26	0.53	37.93	37.38	1.76
4	4	2	262.04	8.77	9.29	0.52	32.88	29.14	1.64
4	4	3	222.69	8.47	8.89	0.50	28.31	27.87	1.59
4	4	4	211.42	10.10	8.33	0.53	29.67	31.19	1.52
Average			268.26	8.97	9.49	0.55	33.26	30.21	1.71
LSD (0.05)*			25.00	NA	0.50	NA	3.00	6.00	NA

*Means within a column which differ by more than the LSD value differ at the 0.05 level of probability

Table A.2 Family means for greenhouse plant height, and field plant height.

Family			Plant Height	
			Greenhouse	Field
			--------Units--------	
set	male	female	cm	cm
1	1	1	8.33	10.81
1	1	2	6.58	9.25
1	1	3	8.57	9.81
1	1	4	7.13	8.66
1	2	1	6.23	7.26
1	2	2	7.25	8.29
1	2	3	7.63	7.17
1	2	4	7.23	9.14
1	3	1	8.08	10.72
1	3	2	9.12	10.97
1	3	3	7.63	8.82
1	3	4	7.25	8.16
1	4	1	8.82	9.74
1	4	2	7.92	9.47
1	4	3	7.97	8.54
1	4	4	8.15	10.00
2	1	1	9.10	9.32
2	1	2	7.82	7.70
2	1	3	7.85	9.52
2	1	4	8.87	9.91
2	2	1	7.97	9.92
2	2	2	7.57	9.45
2	2	3	8.43	8.21
2	2	4	8.17	9.33
2	3	1	8.15	9.57
2	3	2	8.23	9.07
2	3	3	8.68	11.11
2	3	4	7.52	9.05
2	4	1	8.88	9.80
2	4	2	8.23	9.24
2	4	3	7.70	7.49
2	4	4	7.70	10.64
3	1	1	7.88	9.03
3	1	2	8.00	10.69
3	1	3	7.55	9.87
3	1	4	7.63	8.19
3	2	1	7.07	9.38
3	2	2	7.78	9.97

			Plant Height	
			Greenhouse	Field
	Family		--------Units--------	
set	male	female	cm	cm
3	2	3	7.50	9.71
3	2	4	7.72	9.02
3	3	1	7.57	10.87
3	3	2	7.07	9.39
3	3	3	6.78	7.73
3	3	4	6.77	8.71
3	4	1	7.87	9.59
3	4	2	6.83	6.64
3	4	3	7.63	9.86
3	4	4	6.60	8.54
4	1	1	6.60	9.88
4	1	2	7.70	11.06
4	1	3	7.32	10.04
4	1	4	8.02	10.56
4	2	1	7.60	11.35
4	2	2	6.60	9.74
4	2	3	7.05	9.78
4	2	4	6.30	10.39
4	3	1	6.87	9.20
4	3	2	7.47	10.79
4	3	3	7.22	9.46
4	3	4	7.83	9.94
4	4	1	7.58	9.27
4	4	2	7.78	8.66
4	4	3	6.30	10.14
4	4	4	6.65	9.30
Average			7.62	9.42
LSD (0.05)*			0.58	NA

*Means within a column which differ by more than the LSD value differ at the 0.05 level of probability

Table A.3 Family means for raceme number, raceme length, floret number, number of seed, and percent seed set.

Family			Raceme Number	Raceme Length	Floret Number	Seed Number	Percent Seed Set
			----------Units----------				
Set	Male	Female		cm			
1	1	1	2.18	18.30	26.67	7.31	29.28
1	1	2	2.20	16.85	25.50	5.79	23.60
1	1	3	2.18	19.23	26.83	7.94	29.98
1	1	4	2.21	19.28	28.19	5.64	19.26
1	2	1	2.24	18.16	27.57	6.71	24.57
1	2	2	2.15	19.41	27.23	6.92	26.05
1	2	3	2.13	17.97	24.98	6.95	29.43
1	2	4	2.05	18.27	24.44	5.07	20.70
1	3	1	2.13	19.36	28.01	7.01	25.56
1	3	2	2.11	19.97	27.69	8.03	31.08
1	3	3	2.17	18.99	27.87	8.07	29.81
1	3	4	2.17	18.36	28.02	8.06	28.82
1	4	1	2.25	20.69	30.29	6.73	24.83
1	4	2	2.12	19.46	27.47	6.85	25.65
1	4	3	2.22	18.20	27.55	6.79	27.66
1	4	4	2.35	18.84	28.13	5.14	18.95
2	1	1	2.28	19.77	27.12	5.17	20.43
2	1	2	2.08	18.52	24.77	4.48	18.61
2	1	3	2.17	18.25	26.25	5.33	21.30
2	1	4	2.21	18.42	25.65	5.63	23.26
2	2	1	2.29	17.40	26.86	4.68	18.59
2	2	2	2.21	18.55	25.65	5.03	20.87
2	2	3	2.18	18.05	26.89	8.39	33.44
2	2	4	2.34	17.79	28.81	7.73	27.79
2	3	1	2.29	19.03	26.75	4.72	18.63
2	3	2	2.21	17.67	25.63	5.86	23.21
2	3	3	2.01	16.67	22.83	7.12	31.08
2	3	4	2.31	20.13	29.48	7.21	24.95
2	4	1	2.33	18.72	27.53	6.84	26.54
2	4	2	2.27	20.05	28.71	5.83	20.93
2	4	3	2.11	19.03	26.31	5.48	20.89
2	4	4	2.19	18.53	26.12	7.38	29.38
3	1	1	2.23	17.81	28.00	7.26	27.35
3	1	2	2.06	17.81	26.33	8.29	33.63
3	1	3	2.14	17.73	26.46	5.10	20.32
3	1	4	2.10	17.28	24.66	6.45	27.78
3	2	1	2.07	17.43	25.26	4.79	20.93

Family			Raceme Number	Raceme Length	Floret Number	Seed Number	Percent Seed Set
			----------Units----------				
Set	Male	Female		cm			
3	2	2	2.11	19.19	27.56	8.51	33.19
3	2	3	2.19	18.44	29.04	6.63	24.23
3	2	4	2.07	18.87	26.65	9.54	37.28
3	3	1	2.13	18.25	27.03	5.31	20.61
3	3	2	2.15	20.05	29.67	6.99	25.30
3	3	3	2.18	18.45	27.16	5.09	19.74
3	3	4	2.05	18.16	26.23	6.35	26.06
3	4	1	2.36	20.24	32.12	9.18	29.34
3	4	2	2.23	19.33	28.18	5.58	20.55
3	4	3	2.17	18.05	26.93	7.37	29.71
3	4	4	2.13	17.08	25.79	7.31	30.03
4	1	1	2.19	19.52	27.21	7.43	27.84
4	1	2	2.19	18.93	26.95	6.77	26.38
4	1	3	2.16	19.71	28.05	10.21	35.03
4	1	4	2.24	20.15	29.66	8.47	28.91
4	2	1	2.23	18.90	27.67	9.59	36.44
4	2	2	2.18	19.08	26.70	7.57	28.91
4	2	3	2.27	19.35	29.14	8.28	29.97
4	2	4	2.23	18.75	27.95	8.27	29.76
4	3	1	2.23	20.25	29.03	9.63	32.33
4	3	2	2.18	17.77	25.25	6.61	26.19
4	3	3	2.19	17.63	25.57	7.19	28.68
4	3	4	2.34	19.89	30.27	8.89	31.00
4	4	1	2.45	18.25	29.28	7.39	24.96
4	4	2	2.16	18.67	27.20	7.12	26.01
4	4	3	2.12	19.69	27.39	7.10	27.59
4	4	4	2.21	19.00	28.69	9.32	34.13
Average			2.19	18.71	27.26	6.96	26.49
LSD (0.05)*			0.08	0.70	1.90	1.80	6.70

*Means within a column which differ by more than the LSD value differ at the 0.05 level of probability

APPENDIX B

CHAPTER III FAMILY MEANS

Table B.1 Family means for visual color, density, turf quality, spring greenup fall dormancy, percent living cover, percent winter kill, and sensor color.

Family			Visual Color	Density	Turf Quality	Spring Greenup	Fall Dormancy	% Living Cover	% Winter Kill	Sensor Color
set	male	female	----------Visual Rating----------							NDVI
1	1	1	5.80	6.93	6.55	7.33	5.30	96.73	3.83	8.73
1	1	2	6.87	6.77	6.09	6.62	5.26	97.03	7.67	8.45
1	1	3	6.63	7.04	6.40	7.07	5.10	96.23	4.67	9.08
1	1	4	6.66	7.01	6.44	6.91	5.04	91.27	7.41	8.51
1	2	1	7.17	7.13	6.63	6.88	5.52	96.60	9.33	9.36
1	2	2	7.17	6.91	6.36	7.01	4.86	97.13	6.17	9.19
1	2	3	7.00	6.89	6.25	6.87	5.33	94.57	7.50	9.32
1	2	4	6.60	6.89	6.40	7.02	5.56	96.60	7.17	8.73
1	3	1	5.60	6.75	6.12	6.91	5.18	95.83	6.67	8.45
1	3	2	6.10	6.75	6.16	7.05	5.17	96.70	5.00	8.09
1	3	3	6.37	7.11	6.45	7.10	5.43	96.63	5.17	8.82
1	3	4	6.37	6.68	6.12	6.81	5.18	96.47	12.33	8.42
1	4	1	6.33	6.95	6.35	7.12	5.28	95.37	5.33	8.43
1	4	2	6.63	6.85	6.33	6.88	5.31	97.17	5.67	8.85
1	4	3	6.70	6.75	6.17	6.73	5.24	96.13	9.50	8.74
1	4	4	6.53	6.95	6.76	7.13	4.93	97.33	7.17	9.01
2	1	1	6.13	6.49	5.97	6.90	5.45	95.37	7.33	8.59
2	1	2	6.97	6.91	6.29	7.04	5.41	96.73	6.67	9.72
2	1	3	6.27	6.88	6.31	6.61	5.30	96.97	6.67	8.93
2	1	4	6.13	6.97	6.40	7.07	5.09	97.23	4.17	8.75
2	2	1	5.90	7.01	6.59	7.11	5.45	95.20	8.33	8.82
2	2	2	6.80	6.88	6.51	6.89	5.40	96.77	6.00	9.20
2	2	3	6.80	7.08	6.59	7.10	5.47	95.40	7.00	8.57

Family			Visual Color	Density	Turf Quality	Spring Greenup	Fall Dormancy	% Living Cover	% Winter Kill	Sensor Color
2	2	4	6.17	7.09	6.61	6.98	5.36	97.20	4.83	9.38
2	3	1	6.53	6.77	6.19	6.94	5.38	96.90	6.67	9.07
2	3	2	6.27	6.88	6.21	6.73	5.11	96.73	5.50	8.54
2	3	3	6.60	7.08	6.64	7.09	4.98	97.07	3.00	8.35
2	3	4	6.73	6.92	6.39	6.74	5.26	96.67	5.83	9.56
2	4	1	6.23	6.65	6.05	6.98	5.48	95.87	4.83	8.56
2	4	2	7.03	6.88	6.33	6.95	4.96	96.87	4.67	8.80
2	4	3	6.73	7.17	6.76	7.04	5.21	97.53	5.50	9.03
2	4	4	6.67	6.63	6.17	6.65	5.21	95.43	8.50	8.79
3	1	1	6.67	7.25	6.85	7.34	5.24	97.13	4.00	8.92
3	1	2	6.63	6.79	6.36	6.91	5.15	97.47	6.33	8.95
3	1	3	7.10	7.21	6.83	7.18	5.08	98.33	2.83	9.01
3	1	4	7.07	7.31	6.95	7.28	5.43	96.30	2.50	9.30
3	2	1	7.00	7.41	7.07	7.36	5.28	98.27	3.17	9.16
3	2	2	6.57	6.93	6.49	7.08	4.91	97.37	4.00	9.06
3	2	3	6.72	7.13	6.63	7.21	4.77	90.40	5.17	8.69
3	2	4	6.73	6.72	6.16	6.57	5.12	94.50	9.77	8.53
3	3	1	6.97	6.95	6.49	6.90	5.03	97.33	5.50	9.19
3	3	2	6.63	7.23	6.79	7.25	5.11	97.40	4.50	9.30
3	3	3	7.13	6.97	6.41	7.00	5.41	96.63	6.17	9.03
3	3	4	7.07	6.97	6.37	6.51	5.35	95.37	11.33	8.36
3	4	1	6.43	7.04	6.60	7.17	4.93	96.63	5.50	9.33
3	4	2	6.80	6.52	6.01	6.59	5.44	83.63	13.33	7.61
3	4	3	6.73	6.91	6.53	6.99	5.02	97.77	4.17	9.47
3	4	4	7.10	6.98	6.42	6.68	5.02	90.07	12.17	8.79
4	1	1	6.60	6.96	6.44	7.04	5.21	97.30	6.00	8.77

Family			Visual Color	Density	Turf Quality	Spring Greenup	Fall Dormancy	% Living Cover	% Winter Kill	Sensor Color
4	1	2	6.83	7.20	6.71	6.93	5.05	97.33	8.67	9.83
4	1	3	6.80	6.92	6.31	6.73	5.04	94.47	10.67	9.17
4	1	4	6.23	6.91	6.37	7.33	5.23	97.03	3.83	8.62
4	2	1	6.67	7.11	6.25	6.80	5.04	96.40	10.50	8.67
4	2	2	6.70	7.11	6.48	6.99	4.92	97.33	8.00	9.39
4	2	3	6.73	7.05	6.69	7.09	4.97	97.10	7.17	9.23
4	2	4	6.47	7.16	6.59	6.91	4.69	97.50	6.67	9.10
4	3	1	6.80	6.93	6.20	6.87	4.93	96.83	6.83	8.94
4	3	2	6.83	7.00	6.41	6.71	4.62	97.90	9.00	8.95
4	3	3	6.93	7.04	6.55	6.65	4.91	97.30	12.00	9.29
4	3	4	6.87	6.83	6.11	6.72	4.98	96.43	8.17	9.26
4	4	1	6.27	7.19	6.52	7.06	5.04	97.03	7.17	9.09
4	4	2	6.43	6.78	6.31	6.80	5.18	96.10	15.10	9.16
4	4	3	6.63	6.62	5.89	6.42	5.04	91.13	16.17	8.52
4	4	4	6.66	6.94	6.44	6.80	4.90	90.90	9.14	8.66
Average			6.63	6.95	6.42	6.94	5.16	96.01	7.06	8.91
LSD (0.05)*			0.40	0.40	0.30	0.20	0.30	1.30	NA	0.40

*Means within a column which differ by more than the LSD value differ at the 0.05 level of probability

Table B.2 Family means for five dates of turf quality ratings in 2002 and 2003.

			Turf Quality				
	Family		04/27/02	05/21/02	08/26/02	09/28/02	10/18/03
set	male	female	----------Visual Rating----------				
1	1	1	7.20	6.67	6.40	6.87	5.07
1	1	2	5.93	6.87	6.73	7.33	4.87
1	1	3	6.87	6.67	6.93	7.53	5.20
1	1	4	6.40	6.67	6.67	6.87	4.87
1	2	1	6.00	6.73	7.13	7.20	5.40
1	2	2	6.33	6.67	6.80	7.07	4.80
1	2	3	6.27	6.33	7.27	7.87	4.93
1	2	4	6.53	6.60	6.40	6.87	5.07
1	3	1	6.40	6.53	6.53	7.33	5.40
1	3	2	6.87	6.33	6.67	7.00	5.00
1	3	3	6.80	6.40	6.87	7.20	4.87
1	3	4	6.40	6.47	6.87	7.20	4.53
1	4	1	6.80	6.53	6.40	7.13	5.20
1	4	2	6.53	6.07	6.67	7.27	4.87
1	4	3	5.93	6.53	6.60	7.67	4.33
1	4	4	6.93	6.80	6.60	7.20	5.33
2	1	1	6.20	6.20	6.36	6.33	4.64
2	1	2	6.07	6.53	6.87	7.53	5.00
2	1	3	6.07	6.60	6.67	7.20	4.73
2	1	4	7.00	6.60	6.60	7.33	4.93
2	2	1	6.80	6.53	6.73	6.87	6.00
2	2	2	6.40	6.53	6.87	7.87	5.33
2	2	3	6.67	7.20	7.13	7.73	5.27
2	2	4	6.67	6.67	6.71	7.20	5.43
2	3	1	5.93	6.33	6.40	7.40	5.20
2	3	2	6.00	6.20	6.64	7.21	5.21
2	3	3	7.00	6.53	6.73	7.27	5.60
2	3	4	6.40	6.73	6.73	7.67	4.60
2	4	1	6.20	6.00	6.20	6.53	5.53
2	4	2	6.13	6.67	6.53	7.40	5.33
2	4	3	6.53	7.13	6.80	7.47	5.00
2	4	4	5.87	7.00	6.80	7.47	5.47
3	1	1	7.27	6.87	6.40	7.53	5.27
3	1	2	6.60	6.20	6.53	7.00	4.87
3	1	3	6.87	6.87	6.73	7.40	4.93
3	1	4	7.47	6.73	6.73	7.47	5.60
3	2	1	7.40	6.73	7.13	8.07	5.07
3	2	2	6.67	6.93	6.93	7.53	5.00
3	2	3	6.87	6.87	6.53	7.53	5.60

	Family		Turf Quality				
			04/27/02	05/21/02	08/26/02	09/28/02	10/18/03
set	male	female	----------Visual Rating----------				
3	2	4	5.80	6.47	6.73	7.33	4.53
3	3	1	6.47	6.33	6.87	7.67	4.87
3	3	2	6.67	7.00	6.53	7.60	5.47
3	3	3	6.33	6.40	7.07	7.60	4.60
3	3	4	5.73	6.33	7.20	7.13	4.93
3	4	1	7.00	6.53	6.60	7.53	5.27
3	4	2	5.80	6.53	6.27	6.80	4.60
3	4	3	6.40	6.73	6.73	7.33	4.87
3	4	4	6.13	6.47	6.47	7.33	5.20
4	1	1	6.60	6.47	6.93	7.67	5.07
4	1	2	5.67	6.73	6.93	8.00	5.33
4	1	3	5.93	6.53	7.07	7.47	4.40
4	1	4	7.27	6.47	6.27	7.07	5.20
4	2	1	6.00	6.33	6.47	7.40	4.93
4	2	2	6.53	6.53	6.67	7.53	4.87
4	2	3	6.47	6.40	6.73	7.53	5.00
4	2	4	6.33	6.87	7.07	7.87	4.80
4	3	1	5.93	6.40	6.53	7.53	5.13
4	3	2	5.73	6.20	7.00	7.73	4.87
4	3	3	5.67	6.33	6.93	7.13	5.00
4	3	4	5.93	6.53	6.73	7.20	5.20
4	4	1	6.33	6.60	7.20	7.67	5.27
4	4	2	6.27	5.93	6.71	7.07	5.33
4	4	3	5.40	6.07	6.53	6.67	5.20
4	4	4	6.27	6.20	6.87	7.79	5.21
Average			6.41	6.55	6.73	7.35	5.07
LSD (0.05)*			NA	NA	0.40	0.500	0.60

*Means within a column which differ by more than the LSD value differ at the 0.05 level of probability

Table B.3 Family means for eight dates of fall dormancy ratings during fall 2002 and fall 2003.

Family			Fall Dormancy							
			10/22/02	10/31/02	11/11/02	11/21/02	10/26/03	11/02/03	11/08/03	11/15/03
Set	Male	Female	Visual Rating							
1	1	1	5.53	5.13	3.13	2.20	8.60	7.20	5.67	4.93
1	1	2	7.47	6.73	3.00	2.53	8.07	5.87	3.93	4.47
1	1	3	6.13	5.47	2.80	2.53	8.40	6.60	4.60	4.27
1	1	4	5.93	5.43	3.07	2.43	7.79	6.29	4.86	4.57
1	2	1	7.53	6.93	3.73	3.13	7.80	5.60	4.27	5.13
1	2	2	6.33	5.67	2.67	2.07	8.07	5.67	4.00	4.40
1	2	3	7.47	6.67	3.07	2.33	7.87	6.07	4.47	4.73
1	2	4	7.80	6.93	3.87	3.00	7.87	5.87	4.40	4.73
1	3	1	5.80	5.47	3.07	2.47	8.67	6.67	5.00	4.33
1	3	2	5.67	4.80	3.07	2.27	8.53	6.93	5.27	4.80
1	3	3	7.20	6.60	3.00	2.53	8.40	6.47	4.60	4.67
1	3	4	6.53	5.73	3.20	2.67	8.20	6.60	4.33	4.20
1	4	1	5.67	5.07	3.07	2.47	8.53	6.87	5.20	5.33
1	4	2	7.00	6.20	3.47	2.53	8.00	6.07	4.73	4.47
1	4	3	6.87	6.20	3.33	2.73	8.00	5.87	4.47	4.47
1	4	4	5.60	4.93	2.80	2.27	8.07	6.53	4.87	4.40
2	1	1	7.20	6.20	3.40	2.67	8.20	6.47	4.80	4.67
2	1	2	7.80	7.00	3.20	2.47	7.87	5.93	4.47	4.53
2	1	3	7.07	6.40	3.00	2.27	8.20	6.53	4.73	4.20
2	1	4	6.00	5.20	2.40	1.87	8.53	6.80	4.93	5.00
2	2	1	6.60	5.67	3.07	2.40	8.47	7.07	5.47	4.87
2	2	2	7.60	6.73	3.20	2.47	7.60	6.13	4.67	4.80
2	2	3	6.80	6.07	3.07	2.40	8.33	6.73	5.13	5.20
2	2	4	6.60	6.00	3.07	2.60	8.33	6.67	5.07	4.53

			Fall Dormancy							
	Family		10/22/02	10/31/02	11/11/02	11/21/02	10/26/03	11/02/03	11/08/03	11/15/03
Set	Male	Female	----------Visual Rating----------							
2	3	1	6.73	6.00	2.93	2.40	8.47	6.67	4.93	4.87
2	3	2	6.47	5.73	2.87	2.00	7.93	6.40	5.13	4.33
2	3	3	5.53	4.87	2.27	2.07	8.40	6.60	5.07	5.00
2	3	4	6.93	6.20	3.00	2.40	8.07	6.33	4.67	4.47
2	4	1	6.80	5.60	3.20	2.73	8.47	6.67	5.47	4.87
2	4	2	5.87	5.33	2.73	2.13	8.07	6.27	4.73	4.53
2	4	3	6.33	5.73	2.87	2.33	8.53	6.67	4.60	4.60
2	4	4	5.73	5.13	3.27	2.40	8.47	6.73	5.33	4.60
3	1	1	6.40	5.87	3.33	2.53	8.07	6.47	4.87	4.40
3	1	2	6.80	6.07	2.87	2.20	8.13	6.53	4.27	4.33
3	1	3	7.00	6.80	2.73	2.13	7.73	5.60	4.33	4.33
3	1	4	7.40	6.80	3.13	2.60	8.13	6.07	4.47	4.87
3	2	1	7.20	6.60	2.93	2.40	8.00	6.27	4.27	4.53
3	2	2	6.47	5.87	2.60	1.67	8.00	6.13	4.33	4.20
3	2	3	5.21	4.93	2.71	1.79	8.21	6.21	4.86	4.21
3	2	4	7.00	6.53	3.07	2.13	8.00	6.27	4.00	3.93
3	3	1	7.07	6.53	2.80	1.93	7.67	5.87	3.87	4.47
3	3	2	6.07	5.80	3.07	2.20	8.13	6.33	4.80	4.47
3	3	3	7.80	7.40	3.53	2.67	7.60	5.40	4.27	4.60
3	3	4	7.60	6.87	3.53	2.53	7.93	5.87	4.27	4.20
3	4	1	6.00	5.47	2.60	2.00	8.40	6.33	4.67	4.00
3	4	2	7.13	6.93	3.73	2.60	7.93	6.20	4.67	4.33
3	4	3	6.27	6.07	2.60	2.20	8.00	6.27	4.47	4.27
3	4	4	6.57	6.29	3.14	2.21	7.57	5.50	4.36	4.50
4	1	1	6.73	6.00	3.00	2.47	8.13	6.00	4.47	4.87

Family			Fall Dormancy							
			10/22/02	10/31/02	11/11/02	11/21/02	10/26/03	11/02/03	11/08/03	11/15/03
Set	Male	Female	----------Visual Rating----------							
4	1	2	5.87	5.53	2.60	1.80	8.67	6.93	4.40	4.60
4	1	3	6.80	6.07	2.73	1.87	8.20	6.07	4.40	4.20
4	1	4	6.53	5.47	3.13	2.27	8.67	6.60	4.47	4.67
4	2	1	6.40	5.53	2.60	2.07	8.13	6.60	4.60	4.40
4	2	2	6.13	5.53	2.60	2.40	8.27	6.27	4.20	3.93
4	2	3	5.60	5.20	2.87	2.27	8.47	6.60	4.47	4.27
4	2	4	5.67	5.20	2.33	1.40	8.47	6.40	3.93	4.13
4	3	1	5.93	5.33	2.87	2.07	8.40	6.33	4.47	4.07
4	3	2	6.20	5.73	2.33	1.67	7.80	6.13	3.47	3.60
4	3	3	5.87	5.60	2.80	1.80	8.27	6.40	4.33	4.20
4	3	4	6.20	5.40	3.07	2.40	8.33	6.27	4.00	4.13
4	4	1	6.27	5.80	2.27	1.73	8.60	7.00	4.67	4.00
4	4	2	6.27	6.07	2.93	2.07	8.40	6.67	4.60	4.47
4	4	3	6.60	5.53	3.33	2.53	8.13	6.07	3.73	4.40
4	4	4	5.79	5.43	2.50	2.00	8.14	6.00	4.50	4.86
Average			6.52	5.91	2.97	2.29	8.18	6.34	4.58	4.49
LSD (0.05)*			0.30	0.70	0.50	0.40	0.40	0.40	NA	NA

*Means within a column which differ by more than the LSD value differ at the 0.05 level of probability

Table B.4 Family means for inflorescence color, inflorescence density, growth habit, average daily growth, plant diameter, wet plant biomass, and dry plant biomass.

Family			Infloresence Color	Inflorescence Density	Growth Habit	Avg. Daily Growth	Plant Diameter	Fresh Weight Biomass	Dry Weight Biomass
			----------Visual Rating----------			Units			
Set	Male	Female				cm	cm	kg/ha	kg/ha
1	1	1	6.13	6.00	2.93	0.34	83.67	9470.32	4001.03
1	1	2	6.33	6.47	2.53	0.20	68.73	11876.66	4668.11
1	1	3	6.33	6.60	2.33	0.26	96.73	6722.94	2840.64
1	1	4	6.29	6.50	2.21	0.29	65.93	7287.47	3115.21
1	2	1	5.93	7.07	1.67	0.22	66.87	8163.14	3514.06
1	2	2	6.20	6.60	2.07	0.28	70.33	7247.32	2889.31
1	2	3	6.20	6.93	1.93	0.24	73.07	7046.55	2413.01
1	2	4	5.20	7.00	2.27	0.26	78.00	9536.40	4072.23
1	3	1	6.80	6.47	2.93	0.32	97.13	12414.36	5249.69
1	3	2	6.53	6.47	3.00	0.23	99.47	12359.56	5078.22
1	3	3	6.60	6.67	2.33	0.30	74.20	7007.75	2965.47
1	3	4	5.53	6.33	2.27	0.23	78.47	7883.52	2917.43
1	4	1	5.53	6.13	2.80	0.27	93.79	9099.70	3696.00
1	4	2	6.27	6.93	2.67	0.23	87.47	10817.66	4400.85
1	4	3	6.47	6.80	2.13	0.19	77.87	7616.08	3093.96
1	4	4	6.60	6.40	2.53	0.34	85.87	6524.74	2533.87
2	1	1	6.67	7.00	2.73	0.24	105.80	8533.44	3787.55
2	1	2	5.87	7.07	2.13	0.21	82.27	7515.17	3306.24
2	1	3	6.13	6.40	2.47	0.17	89.53	7977.92	3244.81
2	1	4	7.00	6.33	3.00	0.30	88.60	10427.72	3928.71
2	2	1	6.80	6.40	2.33	0.23	89.00	8864.81	3595.27

	Family		Infloresence Color	Inflorescence Density	Growth Habit	Avg. Daily Growth	Plant Diameter	Fresh Weight Biomass	Dry Weight Biomass
			----------Visual Rating----------			Units			
Set	Male	Female				cm	cm	kg/ha	kg/ha
2	2	2	6.13	6.67	2.20	0.24	81.87	10457.54	4102.17
2	2	3	6.53	7.00	2.53	0.17	77.20	6606.68	3054.70
2	2	4	6.53	6.27	2.80	0.21	86.60	9758.85	3938.55
2	3	1	6.13	6.33	2.47	0.21	74.40	8676.81	3138.59
2	3	2	6.00	6.33	2.67	0.26	86.80	8088.36	3490.27
2	3	3	6.73	6.47	2.67	0.26	88.50	10178.41	3948.40
2	3	4	6.40	6.67	2.67	0.29	69.27	9471.20	3455.90
2	4	1	6.67	5.87	3.00	0.15	93.67	11107.82	4635.95
2	4	2	6.73	6.33	2.43	0.26	88.80	8961.49	3494.07
2	4	3	6.33	6.40	2.53	0.28	64.20	8670.14	3589.17
2	4	4	7.47	5.67	2.87	0.28	88.00	12381.51	4858.98
3	1	1	6.53	7.47	2.67	0.25	89.13	9927.19	4227.90
3	1	2	6.87	7.07	2.80	0.20	100.07	11193.26	5219.94
3	1	3	6.40	7.73	1.87	0.20	80.60	10125.60	3663.35
3	1	4	5.93	7.27	2.33	0.24	74.33	7411.51	3637.87
3	2	1	6.40	7.20	1.93	0.24	81.47	8523.20	3410.81
3	2	2	6.67	7.13	2.40	0.17	104.60	12286.82	5496.75
3	2	3	6.64	6.86	2.14	0.22	93.93	10567.67	4801.71
3	2	4	6.00	6.67	2.07	0.23	85.47	9172.26	3220.19
3	3	1	6.53	7.07	2.27	0.20	104.07	12122.31	5246.05
3	3	2	7.07	6.73	2.40	0.29	71.80	10473.70	4789.49
3	3	3	6.00	7.07	1.93	0.21	76.20	12460.35	5284.44
3	3	4	6.40	6.87	1.73	0.24	72.60	9706.97	4602.88

85

Family			Infloresence Color	Inflorescence Density	Growth Habit	Avg. Daily Growth	Plant Diameter	Fresh Weight Biomass	Dry Weight Biomass
			----------Visual Rating----------			Units			
Set	Male	Female				cm	cm	kg/ha	kg/ha
3	4	1	6.80	7.07	2.47	0.26	89.47	8769.04	3824.17
3	4	2	5.93	7.13	1.47	0.19	58.27	8887.56	4372.28
3	4	3	6.27	7.07	2.40	0.16	84.60	11567.18	5099.68
3	4	4	6.07	6.79	1.8	0.25	72.93	10771.99	4792.31
4	1	1	5.80	7.20	2.27	0.26	76.93	11565.15	4650.23
4	1	2	6.80	7.47	2.00	0.35	85.07	11128.09	4967.10
4	1	3	6.80	7.07	2.20	0.20	92.40	9748.04	4096.27
4	1	4	6.80	7.40	3.00	0.33	96.13	9925.01	4277.65
4	2	1	6.00	7.00	2.67	0.26	84.40	11228.35	4621.14
4	2	2	5.67	6.73	2.27	0.27	90.07	11023.49	4268.32
4	2	3	6.47	7.13	2.60	0.26	80.20	11569.98	5117.63
4	2	4	6.53	7.20	2.53	0.20	81.40	8755.61	3746.59
4	3	1	5.60	7.27	2.53	0.28	89.13	9516.39	4220.77
4	3	2	7.13	6.60	2.00	0.25	88.33	12842.79	4349.73
4	3	3	6.80	7.00	2.00	0.28	78.80	7903.98	3430.50
4	3	4	6.27	7.20	2.80	0.27	92.27	9475.11	3814.49
4	4	1	6.20	6.73	2.33	0.26	93.27	10163.00	4277.74
4	4	2	6.00	7.13	2.57	0.23	78.64	10367.81	3974.29
4	4	3	5.47	6.80	2.53	0.25	8.33	9102.22	3857.69
4	4	4	6.21	7.07	2.36	0.20	73.21	10935.46	4760.41
Average			6.35	6.79	2.40	0.24	83.69	9655.77	4017.79
LSD (0.05)*			0.4	0.40	0.40	NA	13.000	2606.00	NA

*Means within a column which differ by more than the LSD value differ at the 0.05 level of probability

APPENDIX C

ANALYSIS OF VARIANCE TABLES

Table C.1 Analysis of variance tables for morphological characteristics.

Stolon Length

Source	df	ms	exp ms	F-test	Variance
Env. (E)	1	12030	$\sigma^2 + 3\sigma^2_{ccs} + 16\sigma^2_{res} + 64s2re + 48\sigma^2_{cs} + 192\sigma^2_{c}$	6.02	52.26
Set (S)	3	8620	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{cs} + 16\sigma^2_{res} + 48\sigma^2_{cs} + 96\sigma^2_{s}$	4.32	69.00
E x S	3	1996	$\sigma^2 + 3\sigma^2_{ccs} + 16\sigma^2_{res} + 48\sigma^2_{cs}$	0.39	0.00
Rep/E	4	29061	$\sigma^2 + 16\sigma^2_{res} + 64\sigma^2_{re}$	5.64**	373.59
Rep/E x S	12	5151	$\sigma^2 + 16\sigma^2_{res}$	8.45**	283.00
Cross/S	60	2382	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{cs}$	2.58**	243.00
Male/S	12	2382	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs} + 24\sigma^2_{ms}$	2.54**	59.25
Female/S	12	1641	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs} + 24\sigma^2_{fs}$	1.78	29.88
M x F/S	36	2641	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs}$	2.86**	286.24
Cross/E x S	60	924	$\sigma^2 + 3\sigma^2_{ccs}$	1.52*	106.00
Residual	240	609	σ^2		609.00
Total	383				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

Number of Nodes

Source	df	ms	exp ms	F-test	Variance
Env. (E)	1	702.14	$\sigma^2 + 3\sigma^2_{ccs} + 16\sigma^2_{res} + 64s2re + 48\sigma^2_{cs} + 192\sigma^2_{c}$	431.24**	3.64
Set (S)	3	12.25	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{cs} + 16\sigma^2_{res} + 48\sigma^2_{cs} + 96\sigma^2_{s}$	7.54	0.11
E x S	3	1.63	$\sigma^2 + 3\sigma^2_{ccs} + 16\sigma^2_{res} + 48\sigma^2_{cs}$	0.48	0.00
Rep/E	4	6.64	$\sigma^2 + 16\sigma^2_{res} + 64\sigma^2_{re}$	2.87	0.07
Rep/E x S	12	2.32	$\sigma^2 + 16\sigma^2_{res}$	2.21	0.08
Cross/S	60	1.28	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{cs}$	1.52	0.07
Male/S			$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs} + 24\sigma^2_{ms}$		
Female/S			$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs} + 24\sigma^2_{fs}$		
M x F/S			$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs}$		
Cross/E x S	60	0.84	$\sigma^2 + 3\sigma^2_{ccs}$	0.81	0.00
Residual	240	1.04	σ^2		1.04
Total	383				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

Number of Internodes

Source	df	ms	exp ms	F-test	Variance
Env. (E)	1	684.00	$\sigma^2 + 3\sigma^2_{ccs} + 16\sigma^2_{rcs} + 64s2re + 48\sigma^2_{cs} + 192\sigma^2_{c}$	476.40**	3.55
Set (S)	3	11.85	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{cs} + 16\sigma^2_{rcs} + 48\sigma^2_{cs} + 96\sigma^2_{s}$	8.26	0.11
E x S	3	1.44	$\sigma^2 + 3\sigma^2_{ccs} + 16\sigma^2_{rcs} + 48\sigma^2_{cs}$	0.44	0.00
Rep/E	4	8.36	$\sigma^2 + 16\sigma^2_{rcs} + 64\sigma^2_{rc}$	5.47**	0.12
Rep/E x S	12	1.53	$\sigma^2 + 16\sigma^2_{rcs}$	2.91*	0.06
Cross/S	60	1.17	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{cs}$	3.09**	0.13
Male/S	12	1.25	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs} + 24\sigma^2_{ms}$	3.30**	0.04
Female/S	12	1.22	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs} + 24\sigma^2_{fs}$	3.21**	0.04
M x F/S	36	1.13	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs}$	2.98**	0.13
Cross/E x S	60	0.38	$\sigma^2 + 3\sigma^2_{ccs}$	0.72	0.00
Residual	240	0.52	σ^2		0.52
Total	383				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

Stem Diameter

Source	df	ms	exp ms	F-test	Variance
Env. (E)	1	1.55	$\sigma^2 + 3\sigma^2_{ccs} + 16\sigma^2_{rcs} + 64s2re + 48\sigma^2_{cs} + 192\sigma^2_{c}$	71.85**	0.01
Set (S)	3	0.06	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{cs} + 16\sigma^2_{rcs} + 48\sigma^2_{cs} + 96\sigma^2_{s}$	2.69	0.00
E x S	3	0.02	$\sigma^2 + 3\sigma^2_{ccs} + 16\sigma^2_{rcs} + 48\sigma^2_{cs}$	0.83	0.00
Rep/E	4	0.06	$\sigma^2 + 16\sigma^2_{rcs} + 64\sigma^2_{rc}$	2.22	0.00
Rep/E x S	12	0.03	$\sigma^2 + 16\sigma^2_{rcs}$	2.63	0.00
Cross/S	60	0.01	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{cs}$	1.03	0.00
Male/S	12		$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs} + 24\sigma^2_{ms}$		
Female/S	12		$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs} + 24\sigma^2_{fs}$		
M x F/S	36		$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs}$		
Cross/E x S	60	0.01	$\sigma^2 + 3\sigma^2_{ccs}$	0.98	0.00
Residual	240	0.01	σ^2		0.01
Total	383				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

Internode Length

Source	df	ms	exp ms	F-test	Variance
Env. (E)	1	6346.00	$\sigma^2 + 3\sigma^2_{ces} + 16\sigma^2_{rcs} + 64s2re + 48\sigma^2_{cs} + 192\sigma^2_{e}$	422.95**	32.97
Set (S)	3	86.99	$\sigma^2 + 3\sigma^2_{ces} + 6\sigma^2_{cs} + 16\sigma^2_{rcs} + 48\sigma^2_{es} + 96\sigma^2_{s}$	5.8	0.75
E x S	3	15.01	$\sigma^2 + 3\sigma^2_{ces} + 16\sigma^2_{rcs} + 48\sigma^2_{cs}$	0.09	0.00
Rep/E	4	556.00	$\sigma^2 + 16\sigma^2_{rcs} + 64\sigma^2_{re}$	15.94**	8.14
Rep/E x S	12	34.91	$\sigma^2 + 16\sigma^2_{rcs}$	2.37*	1.26
Cross/S	60	40.85	$\sigma^2 + 3\sigma^2_{ces} + 6\sigma^2_{cs}$	3.02**	4.55
Male/S	12	18.51	$\sigma^2 + 3\sigma^2_{ces} + 6\sigma^2_{mfs} + 24\sigma^2_{ms}$	1.37	0.21
Female/S	12	32.22	$\sigma^2 + 3\sigma^2_{ces} + 6\sigma^2_{mfs} + 24\sigma^2_{fs}$	2.38*	0.78
M x F/S	36	51.17	$\sigma^2 + 3\sigma^2_{ces} + 6\sigma^2_{mfs}$	3.78**	6.27
Cross/E x S	60	13.53	$\sigma^2 + 3\sigma^2_{ces}$	0.92	0.00
Residual	240	14.71	σ^2		14.71
Total	383				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

Leaf Length

Source	df	ms	exp ms	F-test	Variance
Env. (E)	1	938.15	$\sigma^2 + 2.7\sigma^2_{ces} + 14.4\sigma^2_{rcs} + 57.3s2re + 41.5\sigma^2_{cs} + 165.9\sigma^2_{e}$	6.92	4.84
Set (S)	3	310.27	$\sigma^2 + 2.7\sigma^2_{ces} + 5.3\sigma^2_{cs} + 14.7\sigma^2_{rcs} + 43\sigma^2_{cs} + 84.5\sigma^2_{s}$	2.29	2.07
E x S	3	135.61	$\sigma^2 + 2.7\sigma^2_{ces} + 14.38\sigma^2_{rcs} + 41.5\sigma^2_{es}$	0.33	0.00
Rep/E	4	1251.00	$\sigma^2 + 13.8\sigma^2_{rcs} + 55\sigma^2_{re}$	9.57**	20.37
Rep/E x S	12	130.77	$\sigma^2 + 13.8\sigma^2_{rcs}$	2.48**	5.66
Cross/S	60	129.40	$\sigma^2 + 2.7\sigma^2_{ces} + 5.2\sigma^2_{cs}$	2.33**	14.19
Male/S	12	93.34	$\sigma^2 + 2.7\sigma^2_{ces} + 5.3\sigma^2_{mfs} + 21\sigma^2_{ms}$	1.68	1.80
Female/S	12	139.73	$\sigma^2 + 2.7\sigma^2_{ces} + 5.3\sigma^2_{mfs} + 21\sigma^2_{fs}$	2.51**	4.01
M x F/S	36	137.97	$\sigma^2 + 2.7\sigma^2_{ces} + 5.2\sigma^2_{mfs}$	2.48**	15.80
Cross/E x S	60	55.62	$\sigma^2 + 2.5\sigma^2_{ces}$	1.06	1.16
Residual	240	52.71	σ^2		52.71
Total	383				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

Leaf Width

Source	df	ms	exp ms	F-test	Variance
Env. (E)	1	0.23	$\sigma^2 + 2.7\sigma^2_{ces} + 14.3\sigma^2_{res} + 57.1s2re + 41.3\sigma^2_{es} + 165.2\sigma^2_{e}$	0.03	0.00
Set (S)	3	0.77	$\sigma^2 + 2.8\sigma^2_{ces} + 5.3\sigma^2_{cs} + 14.7\sigma^2_{res} + 43\sigma^2_{es} + 84.2\sigma^2_{s}$	0.86	0.00
E x S	3	0.89	$\sigma^2 + 2.7\sigma^2_{ces} + 14.38\sigma^2_{res} + 41.3\sigma^2_{cs}$	1.57	0.01
Rep/E	4	1.51	$\sigma^2 + 13.8\sigma^2_{res} + 55\sigma^2_{re}$	2.66	0.02
Rep/E x S	12	0.57	$\sigma^2 + 13.8\sigma^2_{res}$	0.71	0.00
Cross/S	60	0.77	$\sigma^2 + 2.7\sigma^2_{ces} + 5.2\sigma^2_{cs}$	0.99	0.00
Male/S	12		$\sigma^2 + 2.7\sigma^2_{ces} + 5.3\sigma^2_{mfs} + 21\sigma^2_{ms}$		
Female/S	12		$\sigma^2 + 2.7\sigma^2_{ces} + 5.3\sigma^2_{mfs} + 21\sigma^2_{fs}$		
M x F/S	36		$\sigma^2 + 2.7\sigma^2_{ces} + 5.2\sigma^2_{mfs}$		
Cross/E x S	60	0.78	$\sigma^2 + 2.5\sigma^2_{ces}$	0.97	0.00
Residual	240	0.80	σ^2		0.80
Total	383				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

Greenhouse Height

Source	df	ms	exp ms	F-test	Variance
Env. (E)	1	1215.00	$\sigma^2 + 3\sigma^2_{ces} + 16\sigma^2_{res} + 64s2re + 48\sigma^2_{es} + 192\sigma^2_{e}$	3328.11**	6.33
Set (S)	3	18.35	$\sigma^2 + 3\sigma^2_{ces} + 6\sigma^2_{cs} + 16\sigma^2_{res} + 48\sigma^2_{es} + 96\sigma^2_{s}$	50.24**	0.19
E x S	3	0.37	$\sigma^2 + 3\sigma^2_{ces} + 16\sigma^2_{res} + 48\sigma^2_{cs}$	0.08	0.00
Rep/E	4	23.12	$\sigma^2 + 16\sigma^2_{res} + 64\sigma^2_{re}$	4.8	0.29
Rep/E x S	12	4.82	$\sigma^2 + 16\sigma^2_{res}$	8.69**	0.27
Cross/S	60	2.09	$\sigma^2 + 3\sigma^2_{ces} + 6\sigma^2_{cs}$	4.10**	0.26
Male/S	12	2.59	$\sigma^2 + 3\sigma^2_{ces} + 6\sigma^2_{mfs} + 24\sigma^2_{ms}$	5.05**	0.08
Female/S	12	1.02	$\sigma^2 + 3\sigma^2_{ces} + 6\sigma^2_{mfs} + 24\sigma^2_{fs}$	2.00*	0.02
M x F/S	36	2.29	$\sigma^2 + 3\sigma^2_{ces} + 6\sigma^2_{mfs}$	4.48**	0.30
Cross/E x S	60	0.51	$\sigma^2 + 3\sigma^2_{ces}$	0.92	0.00
Residual	240	0.56	σ^2		0.56
Total	383				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

Field Height

Source	df	ms	exp ms	F-test	Variance
Env. (E)	1	6144.00	$\sigma^2 + 3\sigma^2_{ces} + 16\sigma^2_{rcs} + 64s2re + 48\sigma^2_{cs} + 192\sigma^2_{c}$	668.00**	31.95
Set (S)	3	13.98	$\sigma^2 + 3\sigma^2_{ces} + 6\sigma^2_{cs} + 16\sigma^2_{rcs} + 48\sigma^2_{cs} + 96\sigma^2_{s}$	1.52	0.05
E x S	3	9.19	$\sigma^2 + 3\sigma^2_{ces} + 16\sigma^2_{rcs} + 48\sigma^2_{cs}$	1.06	0.01
Rep/E	4	11.07	$\sigma^2 + 16\sigma^2_{rcs} + 64\sigma^2_{rc}$	1.28	0.04
Rep/E x S	12	8.64	$\sigma^2 + 16\sigma^2_{rcs}$	6.90*	0.46
Cross/S	60	5.62	$\sigma^2 + 3\sigma^2_{ces} + 6\sigma^2_{cs}$	1.46	0.30
Male/S	12		$\sigma^2 + 3\sigma^2_{ces} + 6\sigma^2_{mfs} + 24\sigma^2_{ms}$		
Female/S	12		$\sigma^2 + 3\sigma^2_{ces} + 6\sigma^2_{mfs} + 24\sigma^2_{fs}$		
M x F/S	36		$\sigma^2 + 3\sigma^2_{ces} + 6\sigma^2_{mfs}$		
Cross/E x S	60	3.84	$\sigma^2 + 3\sigma^2_{ces}$	3.07**	0.86
Residual	240	1.25	σ^2		1.25
Total	383				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

Number of Racemes per Inflorescence

Source	df	ms	exp ms	F-test	Variance
Env. (E)	1	0.43	$\sigma^2 + 3\sigma^2_{ces} + 16\sigma^2_{rcs} + 64s2re + 48\sigma^2_{cs} + 192\sigma^2_{c}$	13.89*	0.002
Set (S)	3	0.12	$\sigma^2 + 3\sigma^2_{ces} + 6\sigma^2_{cs} + 16\sigma^2_{rcs} + 48\sigma^2_{cs} + 96\sigma^2_{s}$	3.95	0.001
E x S	3	0.03	$\sigma^2 + 3\sigma^2_{ces} + 16\sigma^2_{rcs} + 48\sigma^2_{cs}$	3.03	0
Rep/E	4	0.08	$\sigma^2 + 16\sigma^2_{rcs} + 64\sigma^2_{rc}$	8.08**	0.001
Rep/E x S	12	0.01	$\sigma^2 + 16\sigma^2_{rcs}$	0.8	0
Cross/S	60	0.04	$\sigma^2 + 3\sigma^2_{ces} + 6\sigma^2_{cs}$	3.44**	0.005
Male/S	12	0.03	$\sigma^2 + 3\sigma^2_{ces} + 6\sigma^2_{mfs} + 24\sigma^2_{ms}$	2.96**	0.001
Female/S	12	0.07	$\sigma^2 + 3\sigma^2_{ces} + 6\sigma^2_{mfs} + 24\sigma^2_{fs}$	6.09**	0.003
M x F/S	36	0.03	$\sigma^2 + 3\sigma^2_{ces} + 6\sigma^2_{mfs}$	2.72**	0.003
Cross/E x S	60	0.01	$\sigma^2 + 3\sigma^2_{ces}$	0.89	0
Residual	240	0.01	σ^2		0.01
Total	383				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

Average Raceme Length

Source	df	ms	exp ms	F-test	Variance
Env. (E)	1	180.92	$\sigma^2 + 3\sigma^2_{ccs} + 16\sigma^2_{rcs} + 64s2re + 48\sigma^2_{cs} + 192\sigma^2_{c}$	180.12**	0.94
Set (S)	3	9.45	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{cs} + 16\sigma^2_{rcs} + 48\sigma^2_{cs} + 96\sigma^2_{s}$	9.41*	0.09
E x S	3	1.00	$\sigma^2 + 3\sigma^2_{ccs} + 16\sigma^2_{rcs} + 48\sigma^2_{cs}$	1.19	0.00
Rep/E	4	7.05	$\sigma^2 + 16\sigma^2_{rcs} + 64\sigma^2_{rc}$	8.37**	0.1
Rep/E x S	12	0.84	$\sigma^2 + 16\sigma^2_{rcs}$	1.06	0.00
Cross/S	60	4.78	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{cs}$	5.75**	0.66
Male/S	12	4.87	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs} + 24\sigma^2_{ms}$	5.86**	0.17
Female/S	12	3.47	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs} + 24\sigma^2_{fs}$	4.18**	0.11
M x F/S	36	5.18	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs}$	6.24**	0.73
Cross/E x S	60	0.83	$\sigma^2 + 3\sigma^2_{ccs}$	1.04	0.01
Residual	240	0.80	σ^2		0.80
Total	383				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

Number of Florets per Inflorescence

Source	df	ms	exp ms	F-test	Variance
Env. (E)	1	17772.00	$\sigma^2 + 3\sigma^2_{ccs} + 16\sigma^2_{rcs} + 64s2re + 48\sigma^2_{cs} + 192\sigma^2_{c}$	141.58**	92.50
Set (S)	3	26.05	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{cs} + 16\sigma^2_{rcs} + 48\sigma^2_{cs} + 96\sigma^2_{s}$	2.08	0.14
E x S	3	12.52	$\sigma^2 + 3\sigma^2_{ccs} + 16\sigma^2_{rcs} + 48\sigma^2_{cs}$	1.99	0.13
Rep/E	4	25.35	$\sigma^2 + 16\sigma^2_{rcs} + 64\sigma^2_{rc}$	4.04*	0.30
Rep/E x S	12	6.28	$\sigma^2 + 16\sigma^2_{rcs}$	1.35	0.10
Cross/S	60	14.91	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{cs}$	2.72**	1.57
Male/S	12	12.90	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs} + 24\sigma^2_{ms}$	2.35*	0.31
Female/S	12	20.56	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs} + 24\sigma^2_{fs}$	3.75**	0.63
M x F/S	36	13.70	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs}$	2.50**	1.37
Cross/E x S	60	5.48	$\sigma^2 + 3\sigma^2_{ccs}$	1.18	0.27
Residual	240	4.67	σ^2		4.67
Total	383				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

Number of Seed per Inflorescence

Source	df	ms	exp ms	F-test	Variance
Env. (E)	1	3336.00	$\sigma^2 + 3\sigma^2_{ccs} + 16\sigma^2_{rcs} + 64s2re + 48\sigma^2_{cs} + 192\sigma^2_{c}$	843.71**	17.35
Set (S)	3	71.41	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{cs} + 16\sigma^2_{rcs} + 48\sigma^2_{cs} + 96\sigma^2_{s}$	18.06*	0.71
E x S	3	3.95	$\sigma^2 + 3\sigma^2_{ccs} + 16\sigma^2_{rcs} + 48\sigma^2_{cs}$	0.88	0.00
Rep/E	4	47.91	$\sigma^2 + 16\sigma^2_{rcs} + 64\sigma^2_{rc}$	10.64**	0.68
Rep/E x S	12	4.50	$\sigma^2 + 16\sigma^2_{rcs}$	0.91	0.00
Cross/S	60	8.96	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{cs}$	1.76*	0.64
Male/S	12	8.07	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs} + 24\sigma^2_{ms}$	1.58	0.12
Female/S	12	12.91	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs} + 24\sigma^2_{fs}$	2.53**	0.33
M x F/S	36	7.95	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs}$	1.56	0.48
Cross/E x S	60	5.10	$\sigma^2 + 3\sigma^2_{ccs}$	1.03	0.05
Residual	240	4.95	σ^2		4.95
Total	383				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

Percent Seed Set

Source	df	ms	exp ms	F-test	Variance
Env. (E)	1	65240.00	$\sigma^2 + 3\sigma^2_{ccs} + 16\sigma^2_{rcs} + 64s2re + 48\sigma^2_{cs} + 192\sigma^2_{c}$	2636.76**	339.66
Set (S)	3	567.00	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{cs} + 16\sigma^2_{rcs} + 48\sigma^2_{cs} + 96\sigma^2_{s}$	22.94*	5.65
E x S	3	24.74	$\sigma^2 + 3\sigma^2_{ccs} + 16\sigma^2_{rcs} + 48\sigma^2_{cs}$	0.57	0.00
Rep/E	4	649.00	$\sigma^2 + 16\sigma^2_{rcs} + 64\sigma^2_{rc}$	15.04**	9.47
Rep/E x S	12	43.16	$\sigma^2 + 16\sigma^2_{rcs}$	0.64	0.00
Cross/S	60	115.66	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{cs}$	1.72*	8.05
Male/S	12	95.37	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs} + 24\sigma^2_{ms}$	1.42	1.17
Female/S	12	196.43	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs} + 24\sigma^2_{fs}$	2.91**	5.38
M x F/S	36	95.51	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs}$	1.42	4.69
Cross/E x S	60	67.39	$\sigma^2 + 3\sigma^2_{ccs}$	1.00	0.05
Residual	240	67.23	σ^2		67.23
Total	383				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

Table C.2 Analysis of variance tables for turfgrass performance characteristics.

Visual Color Across Environments

Source	df	ms	exp ms	F-test	Variance
Env. (E)	1	22.77	$\sigma^2 + 3\sigma^2_{ccs} + 16\sigma^2_{rcs} + 64s2re + 48\sigma^2_{cs} + 192\sigma^2_{c}$	435.73**	0.12
Set (S)	3	2.25	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{cs} + 16\sigma^2_{rcs} + 48\sigma^2_{cs} + 96\sigma^2_{s}$	43.01**	0.02
E x S	3	0.05	$\sigma^2 + 3\sigma^2_{ccs} + 16\sigma^2_{rcs} + 48\sigma^2_{cs}$	0.31	0.00
Rep/E	4	0.55	$\sigma^2 + 16\sigma^2_{rcs} + 64\sigma^2_{rc}$	3.28*	0.01
Rep/E x S	12	0.17	$\sigma^2 + 16\sigma^2_{rcs}$	0.93	0.00
Cross/S	60	0.61	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{cs}$	2.40**	0.06
Male/S	12	1.05	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs} + 24\sigma^2_{ms}$	4.18**	0.03
Female/S	12	0.84	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs} + 24\sigma^2_{fs}$	3.32**	0.02
M x F/S	36	0.38	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs}$	1.51	0.02
Cross/E x S	60	0.25	$\sigma^2 + 3\sigma^2_{ccs}$	1.41*	0.02
Residual	240	0.18	σ^2		0.18
Total	383				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

Density

Source	df	ms	exp ms	F-test	Variance
Env. (E)	1	154.00	$\sigma^2 + 3\sigma^2_{ccs} + 16\sigma^2_{rcs} + 64s2re + 48\sigma^2_{cs} + 192\sigma^2_{c}$	197.61**	0.80
Set (S)	3	0.93	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{cs} + 16\sigma^2_{rcs} + 48\sigma^2_{cs} + 96\sigma^2_{s}$	1.19	0.00
E x S	3	0.78	$\sigma^2 + 3\sigma^2_{ccs} + 16\sigma^2_{rcs} + 48\sigma^2_{cs}$	0.73	0.00
Rep/E	4	2.79	$\sigma^2 + 16\sigma^2_{rcs} + 64\sigma^2_{rc}$	2.62*	0.03
Rep/E x S	12	1.06	$\sigma^2 + 16\sigma^2_{rcs}$	4.65**	0.05
Cross/S	60	0.49	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{cs}$	1.92**	0.04
Male/S	12	0.53	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs} + 24\sigma^2_{ms}$	2.08*	0.01
Female/S	12	0.59	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs} + 24\sigma^2_{fs}$	2.34**	0.01
M x F/S	36	0.44	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs}$	1.73**	0.03
Cross/E x S	60	0.25	$\sigma^2 + 3\sigma^2_{ccs}$	1.11	0.01
Residual	240	0.23	σ^2		0.23
Total	383				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

Turf Quality Across Environments

Source	df	ms	exp ms	F-test	Variance
Env. (E)	4	133.92	$\sigma^2 + 3\sigma^2_{ces} + 16\sigma^2_{rcs} + 64s2re + 48\sigma^2_{cs} + 192\sigma^2_{c}$	118.16**	0.69
Set (S)	3	2.18	$\sigma^2 + 3\sigma^2_{ces} + 15\sigma^2_{cs} + 16\sigma^2_{res} + 48\sigma^2_{es} + 240\sigma^2_{s}$	1.92	0.00
E x S	12	1.13	$\sigma^2 + 3\sigma^2_{ces} + 16\sigma^2_{rcs} + 48\sigma^2_{cs}$	0.88	0.00
Rep/E	10	2.84	$\sigma^2 + 16\sigma^2_{rcs} + 64\sigma^2_{re}$	2.21*	0.02
Rep/E x S	30	1.28	$\sigma^2 + 16\sigma^2_{res}$	5.07**	0.06
Cross/S	60	0.80	$\sigma^2 + 3\sigma^2_{ces} + 15\sigma^2_{cs}$	2.51**	0.03
Male/S	12	0.91	$\sigma^2 + 3\sigma^2_{ces} + 15\sigma^2_{mfs} + 60\sigma^2_{ms}$	2.85**	0.01
Female/S	12	0.87	$\sigma^2 + 3\sigma^2_{ces} + 15\sigma^2_{mfs} + 60\sigma^2_{fs}$	2.73**	0.01
M x F/S	36	0.74	$\sigma^2 + 3\sigma^2_{ces} + 15\sigma^2_{mfs}$	2.32**	0.03
Cross/E x S	240	0.32	$\sigma^2 + 3\sigma^2_{ces}$	1.26*	0.02
Residual	600	0.25	σ^2		0.25
Total	959				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

Spring Greenup

Source	df	ms	exp ms	F-test	Variance
Env. (E)	9	698.19	$\sigma^2 + 3\sigma^2_{ces} + 16\sigma^2_{rcs} + 64s2re + 48\sigma^2_{cs} + 192\sigma^2_{c}$	910.59**	3.63
Set (S)	3	1.69	$\sigma^2 + 3\sigma^2_{ces} + 30\sigma^2_{cs} + 16\sigma^2_{res} + 48\sigma^2_{es} + 480\sigma^2_{s}$	2.2	0.00
E x S	27	0.77	$\sigma^2 + 3\sigma^2_{ces} + 16\sigma^2_{rcs} + 48\sigma^2_{cs}$	0.95	0.00
Rep/E	20	1.87	$\sigma^2 + 16\sigma^2_{rcs} + 64\sigma^2_{re}$	2.31**	0.02
Rep/E x S	60	0.81	$\sigma^2 + 16\sigma^2_{res}$	3.86**	0.04
Cross/S	60	1.36	$\sigma^2 + 3\sigma^2_{ces} + 30\sigma^2_{cs}$	7.79**	0.04
Male/S	12	1.24	$\sigma^2 + 3\sigma^2_{ces} + 30\sigma^2_{mfs} + 120\sigma^2_{ms}$	7.10**	0.01
Female/S	12	1.59	$\sigma^2 + 3\sigma^2_{ces} + 30\sigma^2_{mfs} + 120\sigma^2_{fs}$	9.06**	0.01
M x F/S	36	1.33	$\sigma^2 + 3\sigma^2_{ces} + 30\sigma^2_{mfs}$	7.59**	0.04
Cross/E x S	540	0.18	$\sigma^2 + 3\sigma^2_{ces}$	0.83	0.00
Residual	1200	0.21	σ^2		0.21
Total	1919				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

Fall Dormancy Across Environments

Source	df	ms	exp ms	F-test	Variance
Env. (E)	7	732.93	$\sigma^2 + 3\sigma^2_{ccs} + 16\sigma^2_{rcs} + 64s2re + 48\sigma^2_{cs} + 192\sigma^2_{e}$	421.66**	3.81
Set (S)	3	6.44	$\sigma^2 + 3\sigma^2_{ccs} + 24\sigma^2_{cs} + 16\sigma^2_{rcs} + 48\sigma^2_{cs} + 384\sigma^2_{s}$	3.71*	0.01
E x S	21	1.73	$\sigma^2 + 3\sigma^2_{ccs} + 16\sigma^2_{rcs} + 48\sigma^2_{cs}$	1.28	0.38
Rep/E	16	3.62	$\sigma^2 + 16\sigma^2_{rcs} + 64\sigma^2_{re}$	2.67**	0.04
Rep/E x S	48	1.35	$\sigma^2 + 16\sigma^2_{rcs}$	5.78**	0.07
Cross/S	60	0.80	$\sigma^2 + 3\sigma^2_{ccs} + 24\sigma^2_{cs}$	1.74**	0.01
Male/S	12	1.02	$\sigma^2 + 3\sigma^2_{ccs} + 24\sigma^2_{mfs} + 96\sigma^2_{ms}$	2.20*	0.01
Female/S	12	0.59	$\sigma^2 + 3\sigma^2_{ccs} + 24\sigma^2_{mfs} + 96\sigma^2_{fs}$	1.27	0.00
M x F/S	36	0.80	$\sigma^2 + 3\sigma^2_{ccs} + 24\sigma^2_{mfs}$	1.74**	0.01
Cross/E x S	420	0.46	$\sigma^2 + 3\sigma^2_{ccs}$	1.97**	0.08
Residual	960	0.23	σ^2		0.23
Total	1535				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

Percent Living Cover

Source	df	ms	exp ms	F-test	Variance
Env. (E)	1	1383.96	$\sigma^2 + 3\sigma^2_{ccs} + 16\sigma^2_{rcs} + 64s2re + 48\sigma^2_{cs} + 192\sigma^2_{e}$	199.94**	7.17
Set (S)	3	25.06	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{cs} + 16\sigma^2_{rcs} + 48\sigma^2_{cs} + 96\sigma^2_{s}$	3.62	0.19
E x S	3	6.92	$\sigma^2 + 3\sigma^2_{ccs} + 16\sigma^2_{rcs} + 48\sigma^2_{cs}$	0.27	0.00
Rep/E	4	55.50	$\sigma^2 + 16\sigma^2_{rcs} + 64\sigma^2_{re}$	2.17	0.47
Rep/E x S	12	25.55	$\sigma^2 + 16\sigma^2_{rcs}$	1.80*	0.71
Cross/S	60	34.81	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{cs}$	13.20**	5.36
Male/S	12	50.71	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs} + 24\sigma^2_{ms}$	19.23**	2.00
Female/S	12	26.05	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs} + 24\sigma^2_{fs}$	9.88**	0.97
M x F/S	36	32.43	$\sigma^2 + 3\sigma^2_{ccs} + 6\sigma^2_{mfs}$	12.30**	4.97
Cross/E x S	60	2.64	$\sigma^2 + 3\sigma^2_{ccs}$	0.19	0.00
Residual	240	14.20	σ^2		14.20
Total	383				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

Percent Winter Kill

Source	df	ms	exp ms	F-test	Variance
Env. (E)	1	15488.92	$\sigma^2 + 3\sigma^2_{ces} + 16\sigma^2_{res} + 64s2re + 48\sigma^2_{cs} + 192\sigma^2_e$	79.32**	79.7
Set (S)	3	186.8	$\sigma^2 + 3\sigma^2_{ces} + 6\sigma^2_{cs} + 16\sigma^2_{res} + 48\sigma^2_{cs} + 96\sigma^2_s$	0.96	0.00
E x S	3	195.27	$\sigma^2 + 3\sigma^2_{ces} + 16\sigma^2_{res} + 48\sigma^2_{cs}$	1.56	1.46
Rep/E	4	200.72	$\sigma^2 + 16\sigma^2_{res} + 64\sigma^2_{re}$	1.61	1.18
Rep/E x S	12	125.03	$\sigma^2 + 16\sigma^2_{res}$	4.39**	6.04
Cross/S	60	43.34	$\sigma^2 + 3\sigma^2_{ces} + 6\sigma^2_{cs}$	1.41	2.09
Male/S	12		$\sigma^2 + 3\sigma^2_{ces} + 6\sigma^2_{mfs} + 24\sigma^2_{ms}$		
Female/S	12		$\sigma^2 + 3\sigma^2_{ces} + 6\sigma^2_{mfs} + 24\sigma^2_{fs}$		
M x F/S	36		$\sigma^2 + 3\sigma^2_{ces} + 6\sigma^2_{mfs}$		
Cross/E x S	60	30.8	$\sigma^2 + 3\sigma^2_{ces}$	1.08	0.78
Residual	240	28.46	σ^2		28.46
Total	383				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

Sensor Color

Source	df	ms	exp ms	F-test	Variance
Env. (E)	1	232.70	$\sigma^2 + 3\sigma^2_{ces} + 16\sigma^2_{res} + 64s2re + 48\sigma^2_{cs} + 192\sigma^2_e$	103.37**	1.2
Set (S)	3	1.26	$\sigma^2 + 3\sigma^2_{ces} + 6\sigma^2_{cs} + 16\sigma^2_{res} + 48\sigma^2_{cs} + 96\sigma^2_s$	0.56	0.00
E x S	3	2.25	$\sigma^2 + 3\sigma^2_{ces} + 16\sigma^2_{res} + 48\sigma^2_{cs}$	9.76**	0.04
Rep/E	4	2.31	$\sigma^2 + 16\sigma^2_{res} + 64\sigma^2_{re}$	10.04**	0.03
Rep/E x S	12	0.23	$\sigma^2 + 16\sigma^2_{res}$	0.57	0.00
Cross/S	60	0.92	$\sigma^2 + 3\sigma^2_{ces} + 6\sigma^2_{cs}$	3.08**	0.10
Male/S	12	0.73	$\sigma^2 + 3\sigma^2_{ces} + 6\sigma^2_{mfs} + 24\sigma^2_{ms}$	2.45*	0.02
Female/S	12	0.95	$\sigma^2 + 3\sigma^2_{ces} + 6\sigma^2_{mfs} + 24\sigma^2_{fs}$	3.17**	0.03
M x F/S	36	0.97	$\sigma^2 + 3\sigma^2_{ces} + 6\sigma^2_{mfs}$	3.26**	0.01
Cross/E x S	60	0.30	$\sigma^2 + 3\sigma^2_{ces}$	0.74	0.00
Residual	240	0.41	σ^2		0.41
Total	383				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

Inflorescence Color

Source	df	ms	exp ms	F-test	Variance
Rep	2	1.69	$\sigma^2 + 16\sigma^2_{rs} + 64s2r$	5.19*	0.02
Set (S)	3	0.94	$\sigma^2 + 3\sigma^2_{cs} + 16\sigma^2_{rs} + 48\sigma^2_{s}$	2.88	0.01
Rep x Set	6	0.33	$\sigma^2 + 16\sigma^2_{rs}$	2.26*	0.01
Cross/S	60	0.55	$\sigma^2 + 3\sigma^2_{cs}$	3.84**	0.14
Male/S	12	0.51	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{ms}$	3.50**	0.03
Female/S	12	0.76	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{fs}$	5.26**	0.05
M x F/S	36	0.50	$\sigma^2 + 3\sigma^2_{mfs}$	3.48**	0.12
Residual	120	0.14	σ^2		0.14
Total	191				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

Inflorescence Density

Source	df	ms	exp ms	F-test	Variance
Rep	2	7.35	$\sigma^2 + 16\sigma^2_{rs} + 64s2r$	15.24**	0.11
Set (S)	3	5.00	$\sigma^2 + 3\sigma^2_{cs} + 16\sigma^2_{rs} + 48\sigma^2_{s}$	10.37**	0.09
Rep x Set	6	0.48	$\sigma^2 + 16\sigma^2_{rs}$	4.27**	0.02
Cross/S	60	0.27	$\sigma^2 + 3\sigma^2_{cs}$	2.43**	0.05
Male/S	12	0.58	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{ms}$	5.09**	0.04
Female/S	12	0.23	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{fs}$	2.04*	0.01
M x F/S	36	0.19	$\sigma^2 + 3\sigma^2_{mfs}$	1.67*	0.03
Residual	120	0.11	σ^2		0.11
Total	191				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

Growth Habit

Source	df	ms	exp ms	F-test	Variance
Rep	2	1.36	$\sigma^2 + 16\sigma^2_{rs} + 64s2r$	2.06	0.01
Set (S)	3	1.45	$\sigma^2 + 3\sigma^2_{cs} + 16\sigma^2_{rs} + 48\sigma^2_{s}$	2.19	0.02
Rep x Set	6	0.66	$\sigma^2 + 16\sigma^2_{rs}$	5.51**	0.03
Cross/S	60	0.32	$\sigma^2 + 3\sigma^2_{cs}$	2.68**	0.07
Male/S	12	0.39	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{ms}$	3.28**	0.02
Female/S	12	0.42	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{fs}$	3.54**	0.03
M x F/S	36	0.26	$\sigma^2 + 3\sigma^2_{mfs}$	2.19**	0.05
Residual	120	0.12	σ^2		0.12
Total	191				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

Average Daily Growth

Source	df	ms	exp ms	F-test	Variance
Rep	2	0.05	$\sigma^2 + 16\sigma^2_{rs} + 64s2r$	4.29	0.001
Set (S)	3	0.02	$\sigma^2 + 3\sigma^2_{cs} + 16\sigma^2_{rs} + 48\sigma^2_{s}$	1.39	0.00
Rep x Set	6	0.01	$\sigma^2 + 16\sigma^2_{rs}$	3.56**	0.00
Cross/S	60	0.005	$\sigma^2 + 3\sigma^2_{cs}$	1.38	0.001
Male/S	12		$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{ms}$		
Female/S	12		$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{fs}$		
M x F/S	36		$\sigma^2 + 3\sigma^2_{mfs}$		
Residual	120	0.003	σ^2		0.003
Total	191				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

Plant Diameter

Source	df	ms	exp ms	F-test	Variance
Rep	2	55.75	$\sigma^2 + 16\sigma^2_{rs} + 64s2r$	0.14	0.00
Set (S)	3	174.98	$\sigma^2 + 3\sigma^2_{cs} + 16\sigma^2_{rs} + 48\sigma^2_{s}$	0.45	0.00
Rep x Set	6	388.13	$\sigma^2 + 16\sigma^2_{rs}$	3.08**	16.39
Cross/S	60	325.79	$\sigma^2 + 3\sigma^2_{cs}$	2.59**	66.63
Male/S	12	363.62	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{ms}$	2.89**	19.81
Female/S	12	200.75	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{fs}$	1.59	6.24
M x F/S	36	354.87	$\sigma^2 + 3\sigma^2_{mfs}$	2.82**	76.32
Residual	120	125.90	σ^2		125.90
Total	191				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

Fresh Weight Biomass

Source	df	ms	exp ms	F-test	Variance
Rep	2	22378570	$\sigma^2 + 16\sigma^2_{rs} + 64s2r$	0.73	0
Set (S)	3	25964030	$\sigma^2 + 3\sigma^2_{cs} + 16\sigma^2_{rs} + 48\sigma^2_{s}$	0.85	0
Rep x Set	6	30453820	$\sigma^2 + 16\sigma^2_{rs}$	5.98**	1586810
Cross/S	60	7652362	$\sigma^2 + 3\sigma^2_{cs}$	1.50*	852503
Male/S	12	5209302	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{ms}$	1.02	9537
Female/S	12	14423417	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{fs}$	2.83**	777380
M x F/S	36	6209697	$\sigma^2 + 3\sigma^2_{mfs}$	1.22	371614
Residual	120	5094853	σ^2		5094853
Total	191				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

Dry Weight Biomass

Source	df	ms	exp ms	F-test	Variance
Rep	2	3840759	$\sigma^2 + 16\sigma^2_{rs} + 64s2r$	0.37	0
Set (S)	3	8561679	$\sigma^2 + 3\sigma^2_{cs} + 16\sigma^2_{rs} + 48\sigma^2_{s}$	0.82	0
Rep x Set	6	10433165	$\sigma^2 + 16\sigma^2_{rs}$	10.15**	587853
Cross/S	60	1405120	$\sigma^2 + 3\sigma^2_{cs}$	1.37	125868
Male/S	12		$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{ms}$		
Female/S	12		$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{fs}$		
M x F/S	36		$\sigma^2 + 3\sigma^2_{mfs}$		
Residual	120	1027517	σ^2		1027517
Total	191				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

9-12-02 Visual Color

Source	df	ms	exp ms	F-test	Variance
Rep	2	0.05	$\sigma^2 + 16\sigma^2_{rs} + 64s2r$	0.67	0.00
Set (S)	3	1.35	$\sigma^2 + 3\sigma^2_{cs} + 16\sigma^2_{rs} + 48\sigma^2_{s}$	18.29**	0.03
Rep x Set	6	0.07	$\sigma^2 + 16\sigma^2_{rs}$	0.34	0.00
Cross/S	60	0.60	$\sigma^2 + 3\sigma^2_{cs}$	2.78**	0.13
Male/S	12	1.10	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{ms}$	5.14**	0.07
Female/S	12	0.78	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{fs}$	3.64**	0.05
M x F/S	36	0.37	$\sigma^2 + 3\sigma^2_{mfs}$	1.73*	0.05
Residual	120	0.21	σ^2		0.21
Total	191				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

10-18-03 Visual Color

Source	df	ms	exp ms	F-test	Variance
Rep	2	1.05	$\sigma^2 + 16\sigma^2_{rs} + 64s2r$	4.01	0.01
Set (S)	3	0.95	$\sigma^2 + 3\sigma^2_{cs} + 16\sigma^2_{rs} + 48\sigma^2_{s}$	3.65	0.01
Rep x Set	6	0.26	$\sigma^2 + 16\sigma^2_{rs}$	1.8	0.01
Cross/S	60	0.26	$\sigma^2 + 3\sigma^2_{cs}$	1.81**	0.04
Male/S	12	0.31	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{ms}$	2.12*	0.01
Female/S	12	0.42	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{fs}$	2.91**	0.02
M x F/S	36	0.19	$\sigma^2 + 3\sigma^2_{mfs}$	1.33	0.01
Residual	120	0.15	σ^2		0.15
Total	191				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

4-27-02 Turf Quality

Source	df	ms	exp ms	F-test	Variance
Rep	2	4.01	$\sigma^2 + 16\sigma^2_{rs} + 64s2r$	1.50	0.02
Set (S)	3	1.84	$\sigma^2 + 3\sigma^2_{cs} + 16\sigma^2_{rs} + 48\sigma^2_{s}$	0.69	0.00
Rep x Set	6	2.66	$\sigma^2 + 16\sigma^2_{rs}$	6.00**	0.14
Cross/S	60	0.59	$\sigma^2 + 3\sigma^2_{cs}$	1.33	0.05
Male/S	12		$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{ms}$		
Female/S	12		$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{fs}$		
M x F/S	36		$\sigma^2 + 3\sigma^2_{mfs}$		
Residual	120	0.45	σ^2		0.45
Total	191				

*Differences were significant (P≤0.05).
**Differences were significant (P≤0.01).

5-21-02 Turf Quality

Source	df	ms	exp ms	F-test	Variance
Rep	2	0.91	$\sigma^2 + 16\sigma^2_{rs} + 64s2r$	2.1	0.01
Set (S)	3	0.68	$\sigma^2 + 3\sigma^2_{cs} + 16\sigma^2_{rs} + 48\sigma^2_{s}$	1.57	0.01
Rep x Set	6	0.43	$\sigma^2 + 16\sigma^2_{rs}$	1.81	0.01
Cross/S	60	0.27	$\sigma^2 + 3\sigma^2_{cs}$	1.13	0.01
Male/S	12		$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{ms}$		
Female/S	12		$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{fs}$		
M x F/S	36		$\sigma^2 + 3\sigma^2_{mfs}$		
Residual	120	0.24	σ^2		0.24
Total	191				

*Differences were significant (P≤0.05).
**Differences were significant (P≤0.01).

8-26-02 Turf Quality

Source	df	ms	exp ms	F-test	Variance
Rep	2	3.56	$\sigma^2 + 16\sigma^2_{rs} + 64s2r$	4.57	0.04
Set (S)	3	1.70	$\sigma^2 + 3\sigma^2_{cs} + 16\sigma^2_{rs} + 48\sigma^2_{s}$	2.18	0.02
Rep x Set	6	0.78	$\sigma^2 + 16\sigma^2_{rs}$	6.24**	0.04
Cross/S	60	0.39	$\sigma^2 + 3\sigma^2_{cs}$	3.14**	0.09
Male/S	12	0.32	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{ms}$	2.53**	0.02
Female/S	12	0.51	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{fs}$	4.06**	0.03
M x F/S	36	0.38	$\sigma^2 + 3\sigma^2_{mfs}$	3.04**	0.09
Residual	120	0.12	σ^2		0.12
Total	191				

*Differences were significant (P≤0.05).
**Differences were significant (P≤0.01).

9-28-02 Turf Quality

Source	df	ms	exp ms	F-test	Variance
Rep	2	4.05	$\sigma^2 + 16\sigma^2_{rs} + 64s2r$	5.70*	0.05
Set (S)	3	2.18	$\sigma^2 + 3\sigma^2_{cs} + 16\sigma^2_{rs} + 48\sigma^2_{s}$	3.07	0.03
Rep x Set	6	0.71	$\sigma^2 + 16\sigma^2_{rs}$	3.26**	0.03
Cross/S	60	0.45	$\sigma^2 + 3\sigma^2_{cs}$	2.06**	0.08
Male/S	12	0.43	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{ms}$	1.98*	0.02
Female/S	12	0.44	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{fs}$	2.01*	0.02
M x F/S	36	0.46	$\sigma^2 + 3\sigma^2_{mfs}$	2.11**	0.08
Residual	120	0.22	σ^2		0.22
Total	191				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

10-18-03 Turf Quality

Source	df	ms	exp ms	F-test	Variance
Rep	2	1.66	$\sigma^2 + 16\sigma^2_{rs} + 64s2r$	0.91	0.00
Set (S)	3	0.31	$\sigma^2 + 3\sigma^2_{cs} + 16\sigma^2_{rs} + 48\sigma^2_{s}$	0.17	0.00
Rep x Set	6	1.82	$\sigma^2 + 16\sigma^2_{rs}$	7.68**	0.10
Cross/S	60	0.37	$\sigma^2 + 3\sigma^2_{cs}$	1.57*	0.04
Male/S	12	0.31	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{ms}$	1.30	0.01
Female/S	12	0.36	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{fs}$	1.51	0.01
M x F/S	36	0.40	$\sigma^2 + 3\sigma^2_{mfs}$	1.69*	0.05
Residual	120	0.24	σ^2		0.24
Total	191				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

10-22-02 Fall Dormancy

Source	df	ms	exp ms	F-test	Variance
Rep	2	0.32	$\sigma^2 + 16\sigma^2_{rs} + 64s2r$	0.19	0.00
Set (S)	3	2.85	$\sigma^2 + 3\sigma^2_{cs} + 16\sigma^2_{rs} + 48\sigma^2_{s}$	1.72	0.02
Rep x Set	6	1.66	$\sigma^2 + 16\sigma^2_{rs}$	1.06*	0.08
Cross/S	60	1.22	$\sigma^2 + 3\sigma^2_{cs}$	3.00**	0.27
Male/S	12	1.71	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{ms}$	4.19**	0.11
Female/S	12	0.83	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{fs}$	2.04*	0.04
M x F/S	36	1.19	$\sigma^2 + 3\sigma^2_{mfs}$	2.92**	0.26
Residual	120	0.41	σ^2		0.41
Total	191				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

10-31-02 Fall Dormancy

Source	df	ms	exp ms	F-test	Variance
Rep	2	1.38	$\sigma^2 + 16\sigma^2_{rs} + 64s2r$	0.99	0.00
Set (S)	3	4.09	$\sigma^2 + 3\sigma^2_{cs} + 16\sigma^2_{rs} + 48\sigma^2_{s}$	2.93	0.06
Rep x Set	6	1.40	$\sigma^2 + 16\sigma^2_{rs}$	3.62**	0.06
Cross/S	60	1.02	$\sigma^2 + 3\sigma^2_{cs}$	2.64**	0.21
Male/S	12	1.34	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{ms}$	3.48**	0.08
Female/S	12	0.58	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{fs}$	1.52	0.02
M x F/S	36	1.06	$\sigma^2 + 3\sigma^2_{mfs}$	2.74**	0.22
Residual	120	0.39	σ^2		0.39
Total	191				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

11-11-02 Fall Dormancy

Source	df	ms	exp ms	F-test	Variance
Rep	2	9.44	$\sigma^2 + 16\sigma^2_{rs} + 64s2r$	14.07**	0.14
Set (S)	3	1.33	$\sigma^2 + 3\sigma^2_{cs} + 16\sigma^2_{rs} + 48\sigma^2_{s}$	1.98	0.01
Rep x Set	6	0.67	$\sigma^2 + 16\sigma^2_{rs}$	3.84**	0.03
Cross/S	60	0.31	$\sigma^2 + 3\sigma^2_{cs}$	1.79**	0.05
Male/S	12	0.24	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{ms}$	1.37	0.005
Female/S	12	0.22	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{fs}$	1.26	0.004
M x F/S	36	0.37	$\sigma^2 + 3\sigma^2_{mfs}$	2.11**	0.07
Residual	120	0.17	σ^2		0.17
Total	191				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

11-21-02 Fall Dormancy

Source	df	ms	exp ms	F-test	Variance
Rep	2	0.64	$\sigma^2 + 16\sigma^2_{rs} + 64s2r$	1.48	0.003
Set (S)	3	1.79	$\sigma^2 + 3\sigma^2_{cs} + 16\sigma^2_{rs} + 48\sigma^2_{s}$	4.12	0.03
Rep x Set	6	0.43	$\sigma^2 + 16\sigma^2_{rs}$	3.59**	0.02
Cross/S	60	0.25	$\sigma^2 + 3\sigma^2_{cs}$	2.03**	0.04
Male/S	12	0.15	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{ms}$	1.23	0.003
Female/S	12	0.13	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{fs}$	1.04	0.001
M x F/S	36	0.32	$\sigma^2 + 3\sigma^2_{mfs}$	2.63**	0.07
Residual	120	0.12	σ^2		0.12
Total	191				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

10-26-03 Fall Dormancy

Source	df	ms	exp ms	F-test	Variance
Rep	2	9.20	$\sigma^2 + 16\sigma^2_{rs} + 64s2r$	15.65**	0.13
Set (S)	3	1.06	$\sigma^2 + 3\sigma^2_{cs} + 16\sigma^2_{rs} + 48\sigma^2_{s}$	1.80	0.01
Rep x Set	6	0.59	$\sigma^2 + 16\sigma^2_{rs}$	5.07**	0.03
Cross/S	60	0.21	$\sigma^2 + 3\sigma^2_{cs}$	1.77**	0.03
Male/S	12	0.23	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{ms}$	1.99*	0.01
Female/S	12	0.32	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{fs}$	2.72**	0.02
M x F/S	36	0.16	$\sigma^2 + 3\sigma^2_{mfs}$	1.38	0.01
Residual	120	0.12	σ^2		0.12
Total	191				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

11-02-03 Fall Dormancy

Source	df	ms	exp ms	F-test	Variance
Rep	2	5.44	$\sigma^2 + 16\sigma^2_{rs} + 64s2r$	4.66	0.07
Set (S)	3	1.73	$\sigma^2 + 3\sigma^2_{cs} + 16\sigma^2_{rs} + 48\sigma^2_{s}$	1.48	0.02
Rep x Set	6	1.17	$\sigma^2 + 16\sigma^2_{rs}$	8.73**	0.07
Cross/S	60	0.39	$\sigma^2 + 3\sigma^2_{cs}$	2.93**	0.08
Male/S	12	0.54	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{ms}$	4.01**	0.03
Female/S	12	0.45	$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{fs}$	3.40**	0.03
M x F/S	36	0.32	$\sigma^2 + 3\sigma^2_{mfs}$	2.42**	0.06
Residual	120	0.13	σ^2		0.13
Total	191				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

11-08-03 Fall Dormancy

Source	df	ms	exp ms	F-test	Variance
Rep	2	0.96	$\sigma^2 + 16\sigma^2_{rs} + 64s2r$	0.29	0.00
Set (S)	3	3.98	$\sigma^2 + 3\sigma^2_{cs} + 16\sigma^2_{rs} + 48\sigma^2_{s}$	1.22	0.00
Rep x Set	6	3.27	$\sigma^2 + 16\sigma^2_{rs}$	11.40**	0.19
Cross/S	60	0.38	$\sigma^2 + 3\sigma^2_{cs}$	1.34	0.03
Male/S	12		$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{ms}$		
Female/S	12		$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{fs}$		
M x F/S	36		$\sigma^2 + 3\sigma^2_{mfs}$		
Residual	120	0.29	σ^2		0.29
Total	191				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

11-15-03 Fall Dormancy

Source	df	ms	exp ms	F-test	Variance
Rep	2	1.54	$\sigma^2 + 16\sigma^2_{rs} + 64s2r$	0.93	0.00
Set (S)	3	1.79	$\sigma^2 + 3\sigma^2_{cs} + 16\sigma^2_{rs} + 48\sigma^2_{s}$	1.09	0.003
Rep x Set	6	1.64	$\sigma^2 + 16\sigma^2_{rs}$	6.61**	0.09
Cross/S	60	0.26	$\sigma^2 + 3\sigma^2_{cs}$	1.04	0.003
Male/S	12		$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{ms}$		
Female/S	12		$\sigma^2 + 3\sigma^2_{mfs} + 12\sigma^2_{fs}$		
M x F/S	36		$\sigma^2 + 3\sigma^2_{mfs}$		
Residual	120	0.25	σ^2		0.25
Total	191				

*Differences were significant (P≤0.05).

**Differences were significant (P≤0.01).

VITA

Kevin Eugene Kenworthy

Doctoral Candidate

Dissertation: QUANTIFICATION OF THE GENETIC VARIATION IN AFRICAN BERMUDAGRASS (*Cynodon transvaalensis)* FOR SELECTED TRAITS

Major Field: Crop Science

Biographical:

Personal Data: Born in Gatesville, Texas, 8 March 1972.

Education: Graduated from Gatesville High School, Gatesville, Texas in May 1990; received Bachelor of Science degree in Agronomy and a Master of Science degree in Crop Science from Texas Tech University, Lubbock, Texas in December 1994 and December 1996 respectively. Completed the requirements for the Doctoral degree with a major in Crop Science at Oklahoma State University in July, 2004.

Experience: Manager of research and development for Thomas Bros. Grass, Ltd., 1997 to 1998; Research Associate in turfgrass breeding and genetics for Texas Agricultural Experiment Station, Dallas, Texas, 1998 to 1999; Instructor of Turfgrass Science for Tarleton State University, 1999 to present; Professor of turfgrass breeding and genetics, University of Florida, beginning June 2004.

Professional Memberships: American Society of Agronomy, Crop Science Society of America, Golf Course Superintendents Association of America.